



CCACGGTCCGGTCAGCTCTGGTTCGGAGAACGAGCGGCTGGCGTGGGCCATCCGGGGAAATGGGC
GCCCTCGTACCTAGTGTGGGGGCAAAAGGGTCTTGCCGGCCTCGCTCGTGAGGGCGTAT
CTGGCGCCTGAGCGGGCGTGGGAGCCCTTGGAGCCCGCAGCAGGGGGCACACCCGGAAACCG
GCCTAGCGCCCGGACCATGAACGGGAGGCCATCTGCGAGGCCCTGCCACCATTCCTTACCA
CAAACTCGCCGACCTGCGCTACCTGAGCCGGGGCCCTCTGGCACTGTGTCGTCGCCGCCACG
CAGACTGGCGCTCCAGGTGGCCGTGAAGCACTGACATCCACACTCCGCTGCTCGACAGTGAA
AGAAAGGATGCTTAAGAGAAAGCTGAAATTTTACACAAAGCTAGATTAGTTACATTCTTCCAAAT
TTTGGGAAATTTGCAATGAGCCTGAAATTTTGGGAATAGTTACTGAATACATGCCAAATGGATCAT
TAAATGAACTCTACATAGGAAACTGAAATATCCTGATGTTGCTTGCCCATTGAGATTTTCGCATC
CTGCATGAAATTTGCCCTTGGTGTAAATTAACCTGCACAAATAGACTCCTCCTTACTTCATCATGA
CTTGAAGACTCAGAAATATCTTATGGCAATGAAATTTTCATGTTAAGATTGCAGATTTTGGTTTAT
CAAAAGTGGCGCATGATGTCCCTCTCACAGTACGAAAGTAGCAAACTCTGCACCCAGAGGGACA
ATTATCTATATGCCACCTGAAACTATGAACCTGGACAAAATCAAGGGCCAGTATCAAGCACGA
TATATAGCTATGCAGTTATCACATGGGAAGTGTATCCAGAAAACAGCCCTTTTGAAGATGTCA
CCAACTCTTGCAGATAATGTATAGTGTGTCAAGAGCATCGACCTGTTATTAATGAAGAAAGT
TTGCCATATGATATACCTCACCGAGCACGTATGATCTCTCTAATAGAAAGTGTGATGGGCACAAA
TCCAGATGAAGACCATCTTTCTTAAATGTTTAAATAGAACTTGAACCAAGTTTGAAGAACATTTG
AAGAGATAACTTTTCTTGAAGCTGTTATTCAGCTAAAGAAACAAAGTTACAGAGTGTTCAGAGT
GCCATTACCTATGTGACAAAGAGAAATGGAAATTAATCTCTGAACATACCTGTAAATCATGTGTC
ACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAATAATAGTGGTTCTCCTGAAACTTCAAGGT
CCCTGCCAGCTCCTGAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAG
CTGCATCACTGTCTGGAAATCAAGTTGGATAGCACCAATTTCTGGATCTCAAGGGCTGCATT
CTGTGATCAAGACCATTCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACT
CAGAACGTCTGGAGCCTGGTATAGCCAGGAGTGGATCCAGAGCAAAAGGAGACATTTGTGAAC
CAAAATGACAGAGCCTGCCCTTAAACCGTCCAGTGTAGTGCCTTCTGTCCAGGACTTGATCATGAA
AGAGGACTATGAACTTGTAGTACCAAGCTTACAAAGGACCTCAAAAGTCAAGACATTAAGTACACA
CTACTGACATCCAGGAGAAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAAACAA
ATGGGTCTTCAGCCTTACCGGAAATATCTTGTGGTTCTAGATCACCATCTTTAAATTTACTTCA
AAATAAAGCATGTAAGTGACTGTTTTCAGAAAGAAATGTGTTTCATAAAGGATATTTATAAA
AAAAAAA

(SEQ ID NO: 1)

FIG. 1

(SEQ ID NO: 2)

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Replacement Sheet

TTTTTATGGG AATCGCAGCT TGGAAGAGAC AGARCAATTC CAGAAWTAAA TTGRAATTGA
AGATTTAACC AATGTTGTTT TAAAATATTC TAACTTCAAA GAATGATGCC AGAACTTWAA
AAGGGRCTGC GCAGAGTAGC AGGGGCCCTG GAGGGCGCGG CCTGAATCCT GATTGCCCTT
CTGCTGAGAG GACACACGCA GCTGAAGATG AATTTGGGAA AAGTAGCCGC TTGCTACTTT
AACTATGGAA GAGCAGGGCC ACAGTGAGAT GGAAATAATC CCATCAGAGT CTCACCCCCA
CATTCAATTA CTGAAAAGCA ATCGGGAAC TCTGGTCACT CACATCCGCA ATACTCAGTG
TCTGGTGGAC AACTTGCTGA AGAATGACTA CTTCTCGGCC GAAGATGCGG AGATTGTGTG
TGCCTGCCCC ACCCAGCCTG ACAAGGTCCG CAAAATTCTG GACCTGGTAC AGAGCAAGGG
CGAGGAGGTG TCCGAGTTCT TCCTCTACTT GCTCCAGCAA CTCGCAGATG CCTACGTGGA
CCTCAGGCCT TGGCTGCTGG AGATCGGCTT CTCCCCTTCC CTGCTCACTC AGAGCAAAGT
CGTGGTCAAC ACTGACCCAG TGAGCAGGTA TACCCAGCAG CTGCGACACC ATCTGGGCCG
TGACTCCAAG TTCGTGCTGT GCTATGCCCA GAAGGAGGAG CTGCTGCTGG AGGAGATCTA
CATGGACACC ATCATGGAGC TGGTTGGCTT CAGCAATGAG AGCCTGGGCA GCCTGAACAG
CCTGGCCTGC CTCCTGGACC ACACCACCGG CATCCTCAAT GAGCAGGGTG AGACCATCTT
CATCCTGGGT GATGCTGGGG TGGGCAAGTC CATGCTGCTA CAGCGGCTGC AGAGCCTCTG
GGCCACGGGC CGGCTAGACG CAGGGGTCAA ATTCTTCTTC CACTTTCGCT GCCGCATGTT
CAGCTGCTTC AAGGAAAGTG ACAGGCTGTG TCTGCAGGAC CTGCTCTTCA AGCACTACTG
CTACCCAGAG CGGGACCCCG AGGAGGTGTT TGCCTTCCTG CTGCGCTTCC CCCACGTGGC
CCTCTTCACC TTCGATGGCC TGGACGAGCT GCACTCGGAC TTGGACCTGA GCCGCGTGCC
TGACAGCTCC TGCCCCTGGG AGCCTGCCCCA CCCCCTGGTC TTGCTGGCCA ACCTGCTCAG
TGGAAGCTG CTCAAGGGGG CTAGCAAGCT GCTCACAGCC CGCACAGGCA TCGAGGTCCC
GCGCCAGTTC CTGCGGAAGA AGGTGCTTCT CCGGGGCTTC TCCCCAGCC ACCTGCGCGC
CTATGCCAGG AGGATGTTCC CCGAGCGGGC CCTGCAGGAC CGCCTGCTGA GCCAGCTGGA
GGCCAACCCC AACCTCTGCA GCCTGTGCTC TGTGCCCCTC TTCTGCTGGA TCATCTTCCG
GTGCTTCCAG CACTTCCGTG CTGCCTTTGA AGGCTCACCA CAGCTGCCCCG ACTGCACGAT
GACCCTGACA GATGTCTTCC TCCTGGTCAC TGAGGTCCAT CTGAACAGGA TGCAGCCCAG
CAGCCTGGTG CAGCGGAACA CACGCAGCCC AGTGGAGACC CTCCACGCCG GCCGGGACAC
TCTGTGCTCG CTGGGGCAGG TGGCCCACCG GGGCATGGAG AAGAGCCTCT TTGTCTTCAC
CCAGGAGGAG GTGCAGGCCT CCGGGCTGCA GGAGAGAGAC ATGCAGCTGG GCTTCCTGCG
GGCTTTGCCG GAGCTGGGCC CCGGGGGTGA CCAGCAGTCC TATGAGTTTT TCCACCTCAC
CCTCCAGGCC TTCTTTACAG CCTTCTTCCT CGTGCTGGAC GACAGGGTGG GCACTCAGGA
GCTGCTCAGG TTCTTCCAGG AGTGGATGCC CCCTGCGGGG GCAGCGACCA CGTCTTGCTA

FIG. 3A

TCCTCCCTTC CTCCCGTTCC AGTGCCTGCA GGGCAGTGGT CCGGCGCGGG AAGACCTCTT
CAAGAACAAG GATCACTTCC AGTTCACCAA CCTCTTCCTG TCGGGGCTGT TGTCCAAAGC
CAAACAGAAA CTCCTGCGGC ATCTGGTGCC CGCGGCAGCC CTGAGGAGAA AGCGCAAGGC
CCTGTGGGCA CACCTGTTTT CCAGCCTGCG GGGCTACCTG AAGAGCCTGC CCCGCGTTCA
GGTCGAAAGC TTCAACCAGG TGCAGGCCAT GCCCACGTTC ATCTGGATGC TCGCTGCAT
CTACGAGACA CAGAGCCAGA AGGTGGGGCA GCTGGCGGCC AGGGGCATCT GCGCCAACTA
CCTCAAGCTG ACCTACTGCA ACGCCTGCTC GGCCGACTGC AGCGCCCTCT CCTTCGTCCT
GCATCACTTC CCCAAGCGGC TGGCCCTAGA CCTAGACAAC AACAATCTCA ACGACTACGG
CGTGCGGGAG CTGCAGCCCT GCTTCAGCCG CCTCACTGTT CTCAGACTCA GCGTAAACCA
GATCACTGAC GGTGGGGTAA AGGTGCTAAG CGAAGAGCTG ACCAAATACA AAATTGTGAC
CTATTTGGGT TTATACAACA ACCAGATCAC CGATGTCGGA GCCAGGTACG TCACCAAAT
CCTGGATGAA TGCAAAGGCC TCACGCATCT TAAACTGGGA AAAAACAAAA TAACAAGTGA
AGGAGGGAAG TATCTCGCCC TGGCTGTGAA GAACAGCAAA TCAATCTCTG AGGTTGGGAT
GTGGGGCAAT CAAGTTGGGG ATGAAGGAGC AAAAGCCTTC GCAGAGGCTC TGCGGAACCA
CCCCAGCTTG ACCACCCTGA GTCTTGCGTC CAACGGCATC TCCACAGAAG GAGGAAAGAG
CCTTGCGAGG GCCCTGCAGC AGAACACGTC TCTAGAAATA CTGTGGCTGA CCCAAAATGA
ACTCAACGAT GAAGTGGCAG AGAGTTTGGC AGAAATGTTG AAAGTCAACC AGACGTAAAA
GCATTTATGG CTTATCCAGA ATCAGATCAC AGCTAAGGGG ACTGCCCAGC TGGCAGATGC
GTTACAGAGC AACACTGGCA TAACAGAGAT TTGCCTAAAT GGAAACCTGA TAAAACCAGA
GGAGGCCAAA GTCTATGAAG ATGAGAAGCG GATTATCTGT TTCTGAGAGG ATGCTTTCCT
GTTTATGGGG TTTTGGCCCT GGAGCCTCAG CAGCAAATGC CACTCTGGGC AGTCTTTTGT
GTCAGTGTCT TAAAGGGGCC TCGCAGGCG GGACTATCAG GAGTCCACTG CCTYCATGAT
GCAAGCCAGC TTCCTGTGCA GAAGGTCTGG TCGGCAAACT CCCTAAGTAC CCGCTACAAT
TCTGCAGAAA AAGAATGTGT CTTGCGAGCT GTTGTAGTTA CAGTAAATAC ACTGTGAAGA
GAAAAA AAAA ACGGACGCGT GG (SEQ ID NO: 7)

FIG. 3B

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCACPTQP
DKVRKILDVLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLEIGFSPSLLTQSKVVVNTDPVSRYT
QQLRHHLGRDSKFVLCYAQKEELLLEEIYMDTIMELVGFSNESLSLACLDDHTTGILNEQG
ETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFHFHRCRMFSCFKESDRCLCLQDLLFKHYCY
PERDPEEVFAFLLRFPHVALFTFDGLDELHSDLDLSRVPDSSCPWEPAPHLVLNLLSGKLLKG
ASKLLTARTGIEVPRQFLRKKVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSV
PLFCWIIIFRCFQHFRAAFEGSPQLPDCMTMTLTDVFLLVTEVHLNRMQPSLLVQRNTRSPVETLHA
GRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALPELPGGDDQSQSYEFFHLTL
QAFFTAFFLVLDLDRVGTQELLRRFFQEWMPAGAAATTSCTCYPPFLPFQCLQSGGPAREDLFKNKDH
QFTNLFCLGLLSKAKQKLLRHLVPAAALRRKRKALWAHLFSSLRGYLKS LPRVQVESFNQVQAMP
TFIWMRLRCIYETQSKVQQLAARGICANYLKLTYCNACSDCSALSFVLHHFPKR LALDLNNDNL
NDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSLELT KYKIVTYLGLYNNQITDVGARYVT KIL
DECKGLTHLKLGNKI TSEGGKYLALAVKNSKSI SEVGMWGNQV GDEGAKAF AEALRNHPSLTTL
SLASNGI STEGGKSLARALQQNTSLEILWLTONELNDEVAESLAEMLKVNQTLKHLWLIQNQITA
KGTAQLADALQSNLTGITEICLNGNLIKPEEAKVYEDEKRIICF (SEQ ID NO: 8) **FIG. 4**

CACGCGTCCGACTTGCTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTGTGT
GTGCTGCCCCACCCAGCCTGACAAGGTCCGCAAAATTCTGGACCTGGTACAGAGCAAG
GGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGCTCCAGCAACTCGCAGATGCCTACGT
GGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCAGTGAGCAGGTATACCCAGCAGCTGCGACACCATCTG
GGCCGTGACTCCAAGTTCGTGCTGTGCTATGCCCAGAAGGAGGAGCTGCTGCTGGAGGA
GATCTACATGGACACCATCATGGAGCTGGTTGGCTTCAGCAATGAGAGCCTGGGCAGCC
TGAACAGCCTGGCCTGCCTCCTGGACCACACCACCGGCATCCTCAATGAGCAGGGTGAG
ACCATCTTCATCCTGGGTGATGCTGGGGTGGGCAAGTCCATGCTGCTACAGCGGCTGCA
GAGCCTCTGGGCCACGGGCCGGCTAGACGCAGGGGTCAAATTCTTCTTCCACTTTCGCT
GCCGCATGTTTCAGCTGCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTC
AAGCACTACTGCTACCCAGAGCGGGACCCCGAGGAGGTGTTTGCCTTCTGCTGCGCTT
CCCCACGTGGCCCTCTTCACCTTCGATGGCCTGGACGAGCTGCACTCGGACTTGGACC
TGAGCCGCGTGCCTGACAGCTCCTGCCCCTGGGAGCCTGCCACCCCCCTGGTCTTGCTG
GCCAACCTGCTCAGTGGGAAGCTGCTCAAGGGGGCTAGCAAGCTGCTCACAGCCCCGCAC
AGGCATCGAGGTCCCGCGCCAGTTCCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCC
CCAGCCACCTGCGCGCCTATGCCAGGAGGATGTTCCCCGAGCGGGCCCTGCAGGACCGC
CTGCTGAGCCAGCTGGAGGCCAACCCCAACCTCTGCAGCCTGTGCTCTGTGCCCTCTT
CTGCTGGATCATCTTCCGGTGCTTCCAGCACTTCCGTGCTGCCTTTGAAGGCTCACCAC
AGCTGCCCCGACTGCACGATGACCCTGACAGATGTCTTCTCCTGGTCACTGAGGTCCAT
CTGAACAGGATGCAGCCAGCAGCCTGGTGCAGCGGAACACACGAGCCAGTGGAGAC
CCTCCACGCCGGCCGGGACACTCTGTGCTCGCTGGGGCAGGTGGCCACCGGGCATGG
AGAAGAGCCTCTTTGTCTTCACCCAGGAGGAGGTGCAGGCCTCCGGGCTGCAGGAGAGA
GACATGCAGCTGGGCTTCTTGCGGGCTTTCGGGAGCTGGGCCCCGGGGGTGACCAGCA
GTCCTATGAGTTTTTCCACCTCAGCCTCCTCACCTGTAAAACTGGGATCCCAGTATAGA
CTTTGGAAATCAGTAGACACCATATGCTTCAAAAAACAGGGGCTATTAAATGACATCA
GGAGCCAGAAAGTCTCATGGCTGTGCTTCTTGAAGTTTATACAACAACCAGATCAC
CGATGTGCGAGCCAGACTGGGAAAAAACAATAACAAGTGAAGGAGGGAAGTATCTCG
CCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTGGGATGTGGGGCAATCAAGTT
GGGATGAAGGAGCAAAAGCCTTCGCAGAGGCTCTGCGGAACCACCCAGCTTGACCAC
CCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCTTGCGAGGGCCC
TGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACTCAACGATGAA
GTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCATTATGGCT
TATCCAGAATCAGATCACAGTCTTTTGTGTGCTGCTTAAAGGGGCTGCGCAGGCGG
GACTATCAGGAGTCCACTGCCTCCATGATGCAAGCCAGCTTCTGTGCAGAAAGTCTGG
TCGGCAAACTCCCTAAGTACCCGCTACAATTCTGCAGAAAAAGAATGTGTCTTGCGAGC
TGTTGTAGTTACAGTAAATACACTGTGAAGAGACTTTATTGCCTATTATAATTATTTT
ATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACAGAGGAGGCCAGCCTCACCTCATTC
CAACACCTGCCATAGGGACCAACGGGAGCGAGTTGGTCACCGCTCTTTTCATTGAAGAG
TTGAGGATGTGGCACAAGTTGGTGCCAAGCTTCTTGAATAAAACGTGTTTGATGGATT
AGTATTATACCTGAAATATTTTCTTCTCTCAGCACTTTCCCATGTATTGATACTGGT
CCCCTTCACAGCTGGAGACACCGGAGTATGTGCAGTGTGGGATTTGACTCCTCCAAGG
TTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGGGCTTTTAATTTTAATCCTG
GAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAGCTCTTAGCTGGTCTAAGA
ATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTCCTCTGCTAGGCTACCCT
CCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTGGGAAGAAGTGATTCTG
TCCCTCCAAAGAAATAGGGCATGGCTTGCCCCCTGTGGCCCTGGCATCCAAATGGCTGCT
TTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCTGCTCCCAAGCAGCTGAAG
GGTGAATAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAAGTGGGCCAGCAGAGCAT
GTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAGGGTGGGGGTGAT
ACTACTAGATCACTTGTCTCTTGGCAGCTCATTTGTTAATAAAATACTGAAAACACAA
AA
AAAAAAAAAAAAAA (SEQ ID NO: 25)

FIG. 5

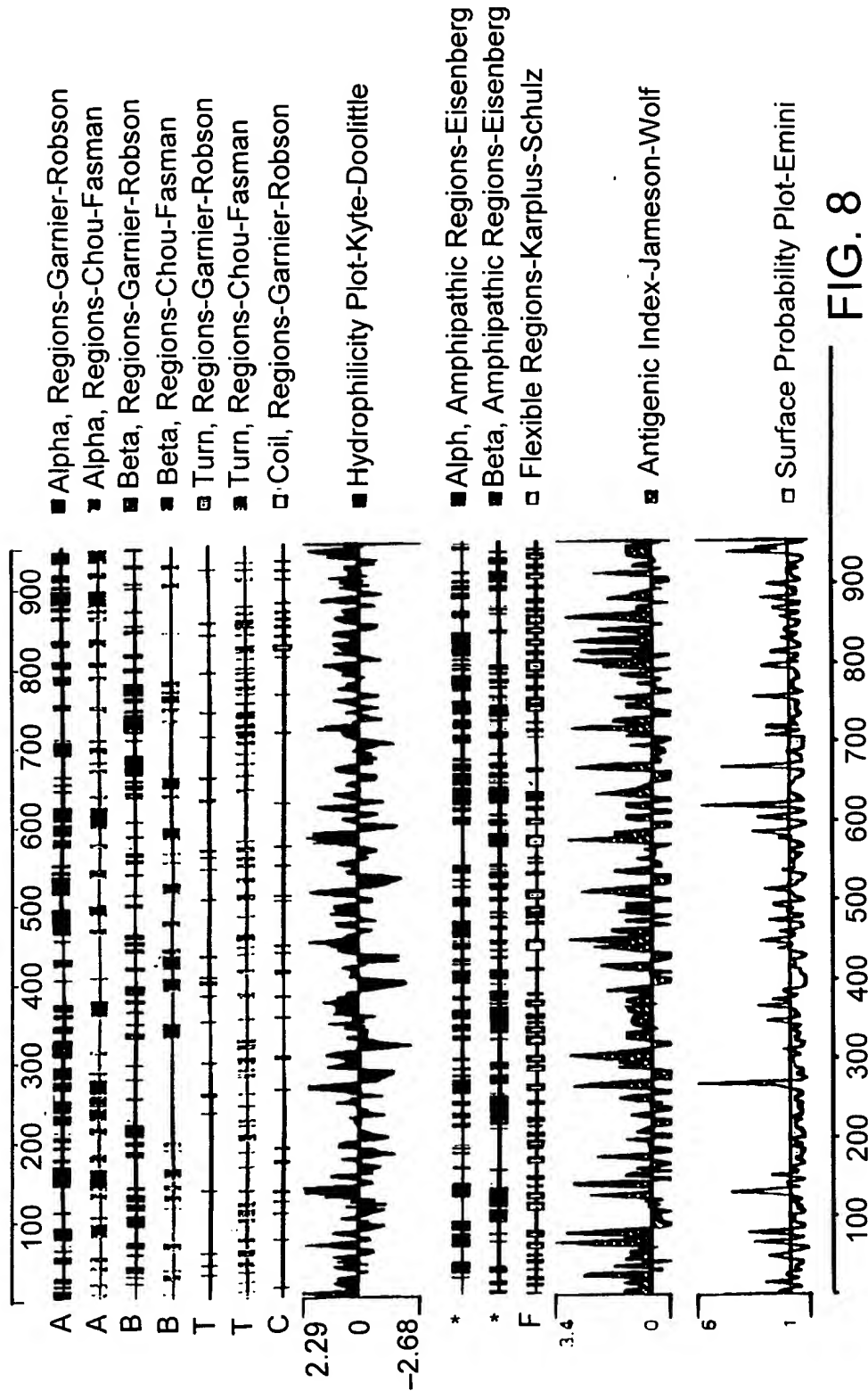
HASDLLKNDYFSAEDAEIVCACPTQPDQKVRKIILDLVQSKGEEVSEFFLYLL
QQLADAYVDLRPWLLLEIGFSPSLLTQSKVVVNTDPVSRYTQQLRHHLGRDS
KFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLSLACLDDHTTGILN
EQGETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFHFRCRMFSCFK
ESDRCLQDLLFKHYCYPERPDEEVFAFLRRFPHVALFTFDGLDELHSDLD
LSRVPDSSCPWEPAHPLVLLANLLSGKLLKGASKLLTARTGIEVPRQFLRK
KVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSVPLFCWI
IFRCFQHFRAAFEGSPQLPDCTMTLTLDVFLLVTEVHLNRMQPSLVQRNTR
SPVETLHAGRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFL
RALPELGPGGDQQSYEFFHLSLLTCKTGIPV (SEQ ID NO: 26)

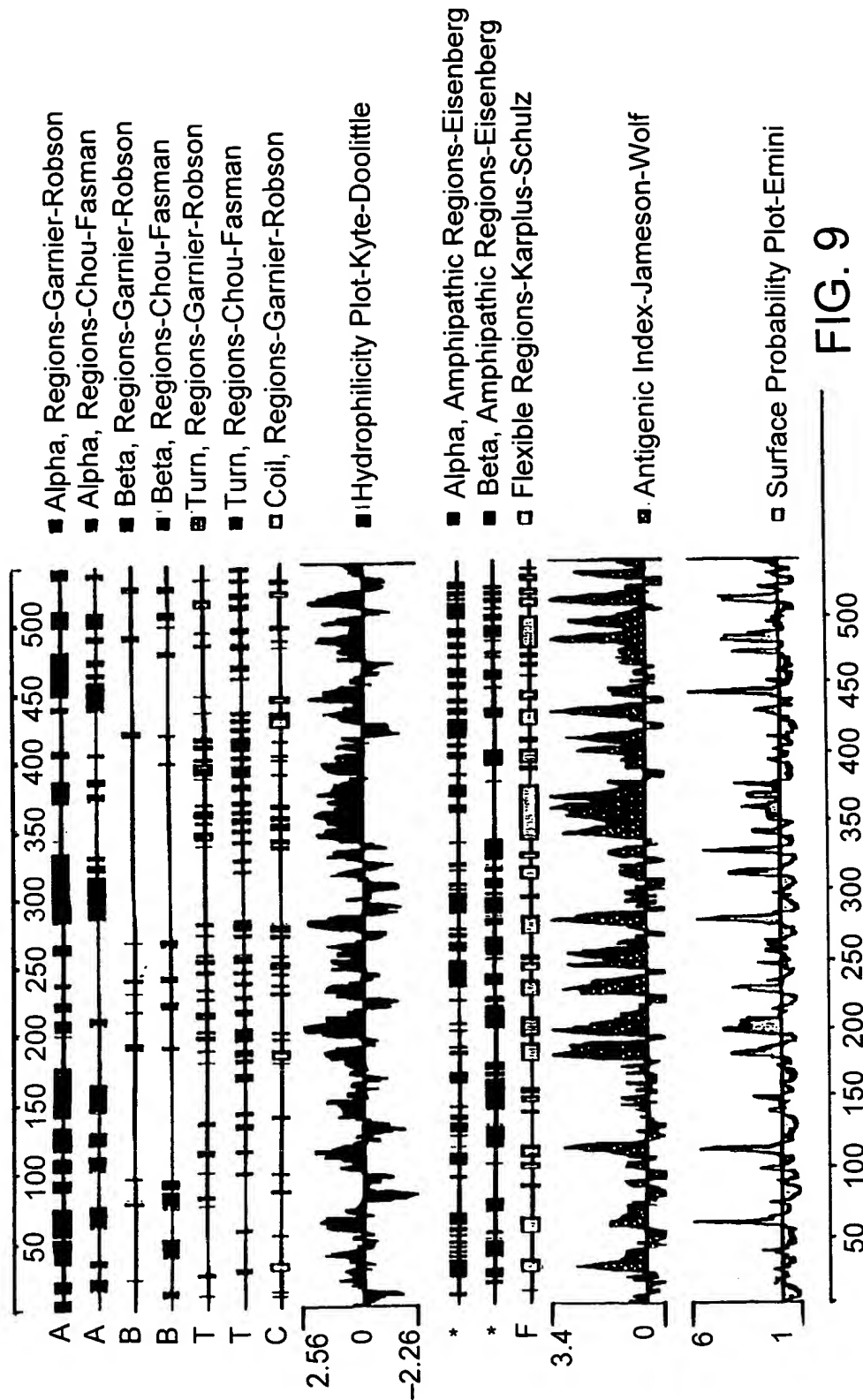
FIG. 6

SEQ. ID NO. 31/32/33/34

1	E	S	H	P	H	I	-	-	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	-	-	-	V	D	N	L	L	K	N	D	Y	CARD4-CARD	
1	L	-	Q	P	G	I	A	Q	Q	W	I	I	Q	S	K	R	E	D	I	V	N	Q	M	T	E	A	-	C	L	N	Q	S	L	D	A	L	L	S	R	D	L	CARD3-CARD
1	A	Q	E	R	-	-	P	S	E	T	I	I	D	R	E	R	K	R	L	V	E	T	L	Q	A	D	S	G	L	I	-	-	L	D	A	L	L	A	R	G	V	ARC-CARD
1	M	A	S	D	D	L	S	-	-	L	I	R	K	N	R	M	A	L	F	Q	Q	L	T	-	-	-	C	V	L	P	I	L	D	N	L	L	K	A	N	V	CIAP1-CARD	
1	K	E	S	N	D	L	L	-	-	L	I	R	K	N	R	M	A	L	F	Q	H	L	T	-	-	-	C	V	I	P	I	L	D	S	L	L	T	A	G	I	CIAP2-CARD	
36	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	E	V	S	E	F	F	L	Y	L	CARD4-CARD	
39	I	M	K	E	D	Y	E	L	V	S	T	K	P	T	R	T	S	K	V	R	Q	L	L	D	T	T	D	I	Q	G	E	E	F	A	K	V	I	V	Q	K	CARD3-CARD	
37	L	T	G	P	E	Y	E	A	L	D	A	L	P	D	A	E	R	R	V	R	L	L	L	L	V	Q	G	K	G	E	A	A	C	Q	E	L	L	R	C	ARC-CARD		
36	I	N	K	Q	E	H	D	I	I	K	Q	K	T	Q	I	P	L	Q	A	R	E	L	I	D	T	I	W	V	K	G	N	A	A	A	A	N	I	F	K	N	C	CIAP1-CARD
36	I	N	E	Q	E	H	D	V	I	K	Q	K	T	Q	T	S	L	Q	A	R	E	L	I	D	T	I	L	V	K	G	N	I	A	A	T	V	E	R	N	S	CIAP2-CARD	
76	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	-	-	L	L	E	I	G	F	S	P	S	L	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CARD4-CARD
79	L	K	D	N	K	Q	-	-	M	G	L	Q	P	Y	P	E	I	L	V	S	R	S	P	S	L	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CARD3-CARD
77	A	Q	R	T	A	G	A	P	D	P	A	W	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ARC-CARD	
76	L	K	E	I	D	S	T	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP1-CARD	
76	L	Q	E	A	E	A	V	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP2-CARD	

FIG. 7





CCCGCGTCCGCGTCCCCGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCT
GCCAAGTCTGTNAACCTGGTGGCCAAGTGATTGTAAGTCAGGAGACTTTCCCTTCGGTTTC
TGCCTTTGATGGCAAGAGGTGGAGATTGTGGCGGCGATTACAGAAAACATCTGGGAAGAC
AAGTTGCTGTTTTTATGGGAATCGCAGGCTTGGAAGAGACAGAAGCAATTCAGAAATAA
ATTGGAAATTGAAGATTTAAACAATGTTGTTTTAAATATTCTAACTTCAAAGAATGATG
CCAGAACTTAAAAAGGGGCTGCGCAGAGTAGCAGGGGCCCTGGAGGGCGCGGCCTGAAT
CCTGATTGCCCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGC
CGCTTGCTACTTTAACTATGGAAGAGCAGGGCCACAGTGAGATGGAAATAATCCCATCAG
AGTCTCACCCCCACATTCAATTACTGAAAAGCAATCGGGAACCTTCTGGTCACTCACATCC
GCAATACTCAGTGTCTGGTGGACAACTTGCTGAAGAATGACTACTTCTCGGCCGAAGATG
CGGAGATTGTGTGTGCCTGCCCCACCCAGCCTGACAAGGTCCGCAAAATTCTGGACCTGG
TACAGAGCAAGGGCGAGGAGGTGTCCGAGTTCTTCCTCTACTTGCTCCAGCAACTCGCAG
ATGCCTACGTGGACCTCAGGCCTTGCTGCTGGAGATCGGCTTCTCCCCTTCCCTGCTCA
CTCAGAGCAAAGTCGTGGTCAACACTGACCCAGTGAGCAGGTATACCCAGCAGCTGCGAC
ACCATCTGGGCCGTGACTCCAAGTTCGTGCTGTGCTATGCCCAGAAGGAGGAGCTGCTGC
TGGAGGAGATCTACATGGACACCATCATGGAGCTGGTTGGCTTCAGCAATGAGAGCCTGG
GCAGCCTGAACAGCCTGGCCTGCCTCCTGGACCACACCACCGGCATCCTCAATGAGCAGG
CTGCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTCAAGCACTACTGCTA
CCCAGAGCGGGACCCCGAGGAGGTGTTTGCTTCTGCTGCGCTTCCCCACGTGGCCCT
CTTACCTTCGATGGCCTGGACGAGCTGCACTCGGACTTGACCTGAGCCGCGTGCCTGA
CAGCTCCTGCCCCCTGGGAGCCTGCCCACCCCCTGGTCTTGCTGGCCAACCTGCTCAGTGG
GAAGCTGCTCAAGGGGGCTAGCAAGCTGCTCACAGCCCGCACAGGCATCGAGGTCCCGCG
CCAGTTCCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCCCAGCCACCTGCGCGCCTA
TGCCAGGAGGATGTTCCCCGAGCGGGCCCTGCAGGACCGCCTGCTGAGCCAGCTGGAGGC
CAACCCCAACCTCTGCAGCCTGTGCTCTGTGCCCTCTTCTGCTGGATCATCTTCCGGTG
CTTCCAGCACTTCCGTGCTGCCTTTGAAGGCTCACACAGCTGCCCCACTGCACGATGAC
CCTGACAGATGTCTTCTCCTGGTCACTGAGGTCCATCTGAACAGGATGCAGCCCAGCAG
CCTGGTGCAGCGGAACACACGCAGCCCAGTGAGACCCTCCACGCCGGCCGGGACACTCT
GTGCTCGCTGGGGCAGGTGGCCCAACGGGGCATGGAGAAGAGCCTCTTTGTCTTCACCCA
GGAGGAGGTGCAGGCCTCCGGGCTGCAGGAGAGAGACATGCAGCTGGGCTTCTGCGGGC
TTTGCCGGAGCTGGGCCCCGGGGGTGACCAGCAGTCCTATGAGTTTTTCCACCTCACCT

FIG. 10A

CCAGGCCTTCTTTACAGCCTTCTTCCTCGTGTGGACGACAGGGTGGGCACTCAGGAGCT
GCTCAGGTTCTTCCAGGAGTGGATGCCCCCTGCGGGGGCAGCGACCACGTCCTGCTATCC
TCCCTTCTCCCGTTCCAGTGCCTGCAGGGCAGTGGTCCGGCGCGGGAAGACCTCTTCAA
GAACAAGGATCACTTCCAGTTCACCAACCTCTTCCTGTGCGGGCTGTTGKCCAAAGCCAA
ACAGAAACTCCTGCGGCATCTGGTGCCCGCGGCAGCCCTGAGGAGAAAGCGCAAGGCCCT
GTGGGCACACCTGTTTTCCAGCCTGCGGGGCTACCTGAAGAGCCTGCCCCGCGTTCAGGT
CGAAAGCTTCAACCAGGTGCAGGCCATGCCCACGTTTCATCTGGATGCTGCGCTGCATCTA
CGAGACACAGAGCCAGAAGGTGGGGCAGCTGGCGGCCAGGGGCATCTGCGCCAACTACCT
CAAGCTGACCTACTGCAACGCCTGCTCGGCCGACTGCAGCGCCCTCTCCTTCGTCCTGCA
TCACTTCCCCAAGCGGCTGGCCCTAGACCTAGACAACAACAATCTCAACGACTACGGCGT
GCGGGAGCTGCAGCCCTGCTTCAGCCGCCTCACTGTTCTCAGACTCAGCGTAAACCAGAT
CACTGACGGTGGGGTAAAGGTGCTAAGCGAAGAGCTGACCAAATACAAAATTGTGACCTA
TTTGGGTTTATACAACAACCAGATCACCGATGTCGGAGCCAGGTACGTCACCAAAATCCT
GGATGAATGCAAAGGCCTCACGCATCTTAAACTGGGAAAAAACAAAATAACAAGTGAAGG
AGGGAAGTATCTCGCCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTTGGGATGTG
GGGCAATCAAGTTGGGGATGAAGGAGCAAAGCCTTCGCAGAGGCTCTGCGGAACCACCC
CAGCTTGACCACCCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCT
TGCGAGGGCCCTGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACT
CAACGATGAAGTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCA
TTTATGGCTTATCCAGAATCASATCACAGCTWARGGGACTGCCCAGCTGGCAGATGCGTT
ACAGAGCAACACTGGCATAACAGAGATTTGCCTAAATGGAAACCTGATAAAACCAGAGGA
GGCCAAAGTCTATGAAGATGAGAAGCGGATTATCTGTTTCTGAGAGGATGCTTTCTCTGTT
CATGGGGTTTTTGGCCCTGGAGCCTCAGCAGCAAATGCCACTYTGGGCAGTCTTTTGTGTC
AGTGTCTTAAAGGGGCTGCGCAGGCGGGACTATCAGGAGTCCACTGCCTCCATGATGCA
AGCCAGCTTCCTGTGCAGAAGGTCTGGTCGGCAAACCTCCCTAAGTACCCGCTACAATTCT
GCAGAAAAAGAATGTGTCTTGCGAGCTGTTGTAGTTACAGTAAATACACTGTGAAGAGAC
TTTATTGCCTATTATAATTATTTTTATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACA
GAGGAGGCCAGCCTCACCTCATTCACACCTGCCATAGGGACCAACGGGAGCGAGTTGG
TCACCGCTCTTTTCATTGAAGAGTTGAGGATGTGGCACAAAGTTGGTGCCAAGCTTCTTG
AATAAAACGTGTTTGATGGATTAGTATTATACCTGAAATATTTTCTTCCTTCTCAGCACT
TTCCCATGTATTGATACTGGTCCCACTTCACAGCTGGAGACACCGGAGTATGTGCAGTGT
GGGATTTGACTCCTCCAAGGTTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGG

FIG. 10B

GCTTTTAATTTTAATCCTGGAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAG
CTCTTAGCTGGTCTAAGAATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTC
CTCTGCTAGGCTACCCTCCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTG
GGAAGAAGTGATTCTGTCCCTCCAAAGAAATAGGGCATGGCTTGCCCCTGTGGCCCTGGC
ATCCAAATGGCTGCTTTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCCTGCCTC
CCAAGCAGCTGAAGGGTGACTAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAACTGG
GCCAGCAGAGCATGTTGGACACCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAG
GGTGGGGGTGATACTACTAGATCACTTGTCTCTTGCCAGCTCATTGTTAATAAAATAC
TGAAAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGG (SEQ ID NO:39)

FIG. 10C

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLEIGFSPSLLTQSKVV
VNTDPVSRYTQQLRHHLGRDSKFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLSL
ACLLDHTTGILNEQAASRKVTGCVCRTCSSSTTATQSGTPRRCLPSCCASPTWPSSPSMA
WTSCRTWT (SEQ ID NO:40)

FIG. 11

CACGCGTCCGCGCTACTGCGGGAGCAGCGTCCTCCCGGGCCACGGCGCTTCCCGGCCCCG
GCGTCCCCGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCTGCGAAGTCT
GTAAACCTGGTGGCCAAGTGATTGTAAGTCAGGAGACTTTCCTTCGGTTTCTGCCTTTGA
TGGCAAGAGGTGGAGATTGTGGCGGCGATTACAGAAAAATCTGGGAAGACAAGTTGCTG
TTTTTATGGGAATCGCAGGCTTGAAGAGACAGAAGCAATTCCAGAAATAAATTGGAAAT
TGAAGATTTAAACAATGTTGTTTTTAAATATTCTAACTTCAAAGAATGATGCCAGAACT
TAAAAAGGGGCTGCGCAGAGTAGCAGGGGCCCTGGAGGGCGCGGCCTGAATCCTGATTGC
CCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGCCGCTTGCTA
CTTTAACTATGGAAGAGCAGGGCCACAGTGAGATGGAAATAATCCCATCAGAGTCTCACC
CCCACATTCAATTACTGAAAAGCAATCGGGAACCTTCTGGTCACTCACATCCGCAATACTC
AGTGTCTGGTGGACAACCTTGCTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTG
TGTGTGCCTGCCCCACCCAGCCTGACAAGGTCCGCAAAATTCTGGACCTGGTACAGAGCA
AGGGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGCTCCAGCAACTCGCAGATGCCTACG
TGGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCCAGGTAGGAGTCAGCCCCAGCAAGACCGCAGGCACCAGT
GCAAGCAGGGCCCTGGGGGGTTTGGTAATGGCTGGGCCAGCCCTGAGTGCCACCTCAGGA
AGCAGGCCCAGGTGCTATTTTGAATTTAGAAAGGAACAGCTGAATCCTGTCTCCCAAGTG
CAGCCCAGGTGGCTGCGATTGAACTGCCCCACACCTCGATGGTCTGGTTTATAGAGGGGCC
TTTGGAAGTATGGGAATGGCCTGTGTTCTGACCCCTTGCTTTCTTCTCCTATTCTGACATAT
GTAGACATTTTAATGGTTGCACAAATTCAGGTTGTATTTTTTTTTCTTTAAAAAAATCT
TTAGCTGGACATGGTAGCACACACCTGTAGTTCCAGCTACTCAGGAGGCTGAGGCAAGAG
GACTGCTTGAGCCCCAGAGTCTAAGGCTGCAGCGAGCTATGATTGTGCCCCTACACTCCA
CAGCCTGGGTTTTAGAGTGAGACCCTGTCTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAANGGGCGG (SEQ ID NO:41)

FIG. 12

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLEIGFSPSLLTQSKVV
VNTDPGRSQPQQDRRHQCKQGPGGFGNGWASPECHLRKQAQVLF
(SEQ ID NO:42)

FIG. 13

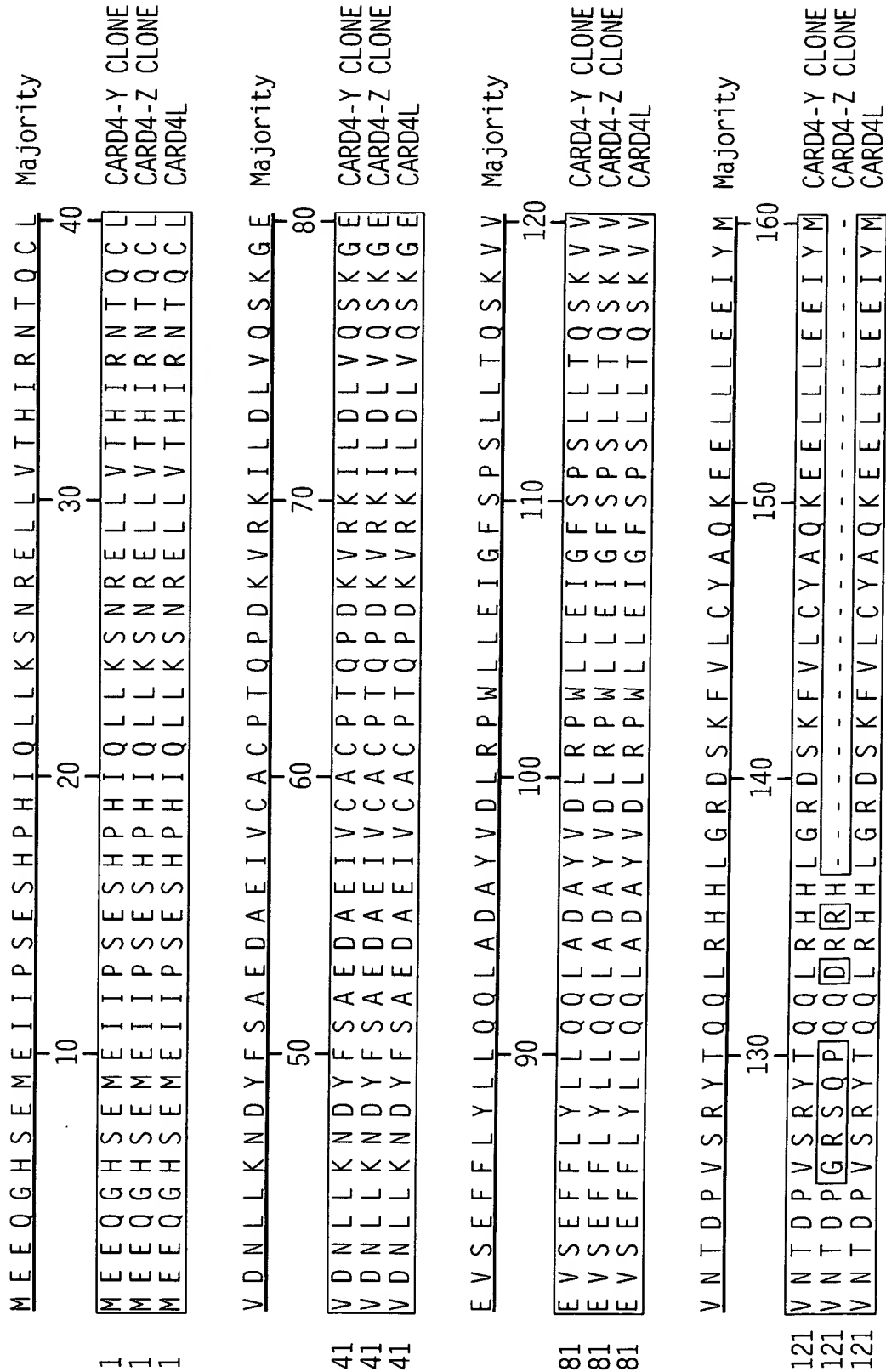
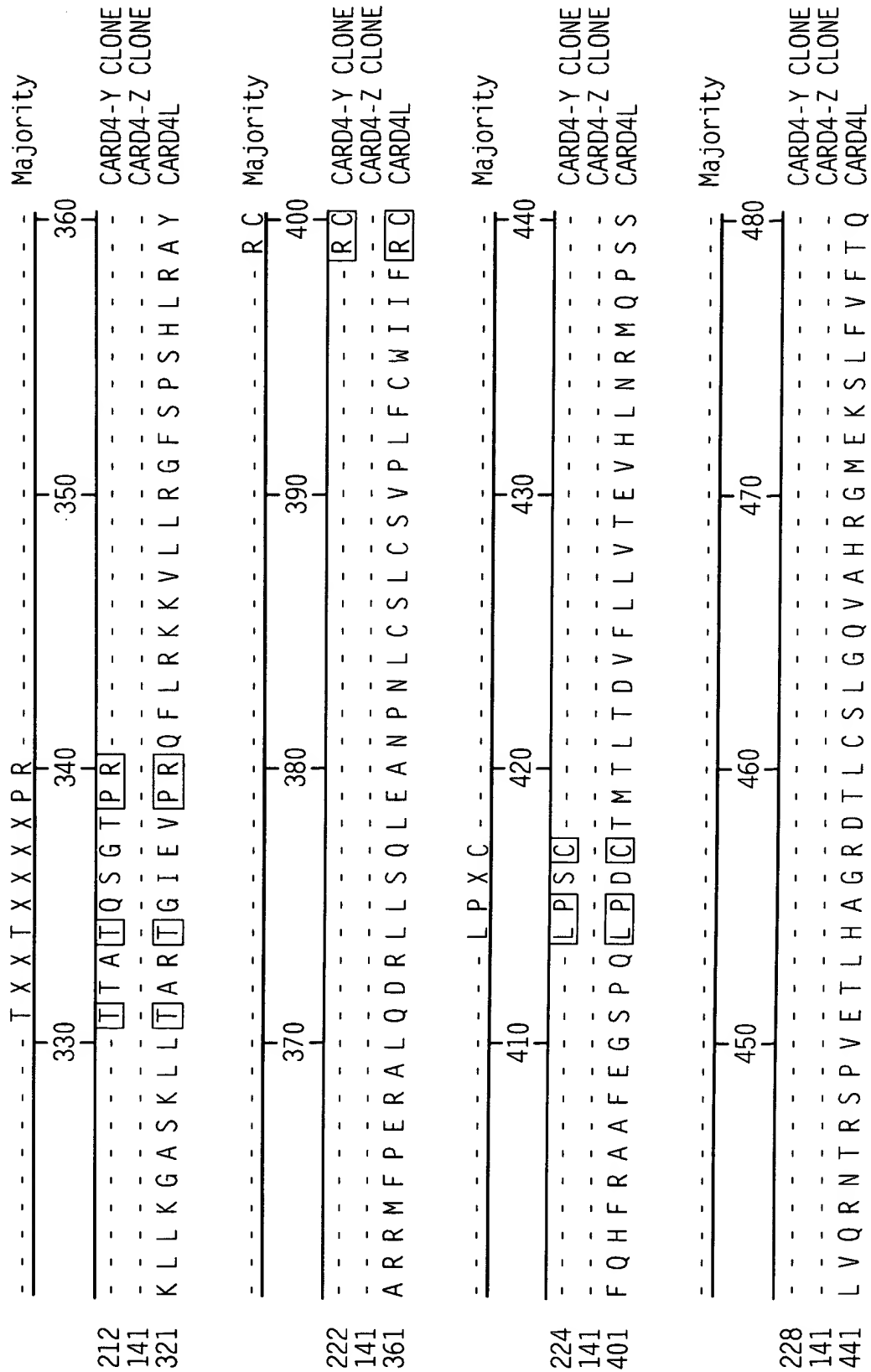
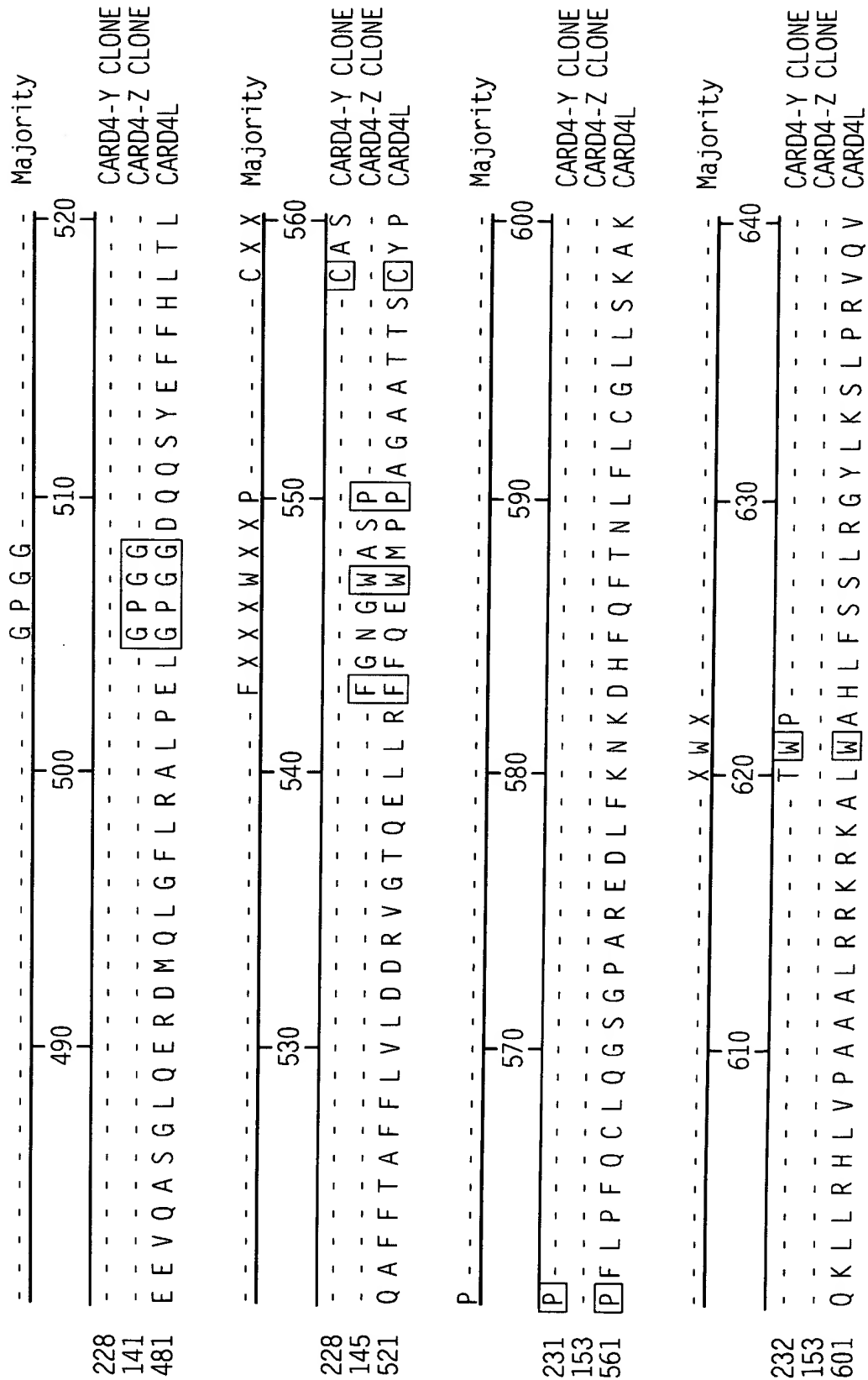


FIG. 14A

	Majority	CARD4-Y CLONE	CARD4-Z CLONE	CARD4L
161	DTIMELVGFSNESLGSLSLACLLDHTTGILN	DTIMELVGFSNESLGSLSLACLLDHTTGILN	DTIMELVGFSNESLGSLSLACLLDHTTGILN	DTIMELVGFSNESLGSLSLACLLDHTTGILN
137	EQXX	EQAA	EQAA	EQAA
161	EQXX	EQAA	EQAA	EQAA
199	LGDAVGKSMLLQRLQSLWATGRLDAGVKFFHFR	LGDAVGKSMLLQRLQSLWATGRLDAGVKFFHFR	LGDAVGKSMLLQRLQSLWATGRLDAGVKFFHFR	LGDAVGKSMLLQRLQSLWATGRLDAGVKFFHFR
137	CR	CR	CR	CR
201	CR	CR	CR	CR
203	CT	CT	CT	CT
141	CT	CT	CT	CT
241	CT	CT	CT	CT
206	FTFDGLDELHSDLDLSRVPDSSCPWEP	FTFDGLDELHSDLDLSRVPDSSCPWEP	FTFDGLDELHSDLDLSRVPDSSCPWEP	FTFDGLDELHSDLDLSRVPDSSCPWEP
141	FTFDGLDELHSDLDLSRVPDSSCPWEP	FTFDGLDELHSDLDLSRVPDSSCPWEP	FTFDGLDELHSDLDLSRVPDSSCPWEP	FTFDGLDELHSDLDLSRVPDSSCPWEP
281	FTFDGLDELHSDLDLSRVPDSSCPWEP	FTFDGLDELHSDLDLSRVPDSSCPWEP	FTFDGLDELHSDLDLSRVPDSSCPWEP	FTFDGLDELHSDLDLSRVPDSSCPWEP





	- - - - X X P X X X W - - - -	650	660	670	680	Majority
235	- - - - S S [P] S M A [W] - - - -					CARD4-Y CLONE
153	- - - - - - - - - - - - - - - -					CARD4-Z CLONE
641	E S F N Q V Q A M [P] T F I [W] M L R C I Y E T Q S Q K V G Q L A A R G I C A N Y L					CARD4L
	- - - - X X C X X X - - - -	690	700	710	720	Majority
242	- - - - T S [C] T R T - - - -					CARD4-Y CLONE
153	- - - - - - - - - - - - - - - -					CARD4-Z CLONE
681	K L T Y C N A [C] S A D C S A L S F V L H H F P K R L A L D L D N N N L N D Y G V					CARD4L
	- - - - - - - - - - - - - - - -	730	740	750	760	Majority
248	- - - - - - - - - - - - - - - -					CARD4-Y CLONE
153	- - - - - - - - - - - - - - - -					CARD4-Z CLONE
721	R E L Q P C F S R L T V L R L S V N Q I T D G G V K V L S E E L T K Y K I V T Y					CARD4L
	- - - - - - - - - - E C X - - - -	770	780	790	800	Majority
248	- - - - - - - - - - - - - - - -					CARD4-Y CLONE
153	- - - - - - - - - - - - - - - -					CARD4-Z CLONE
761	L G L Y N N Q I T D V G A R Y V T K I L D [E C H] [E C K] G L T H L S L Y N N Q I T D V G					CARD4L

[illegible]

	X	X	X	X	F		Majority
249							
164	-	-	-	-	F		CARD4-Y CLONE
961	R	I	I	C	F		CARD4-Z CLONE
							CARD4L

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 14G

CCACGCGTCCGCGGACCGCGAGCGGTAGCGCCCTCCCTCCCAGCTGTTGTCCCGCCCGAT
CCGCGACCCTAGTCCCCGGATCCCCTTGCTGAGAGTCACCGTACTCCAGGGCCAACTGAG
CCAAAGTCCTGCCAACTTGGGTGAGCAATGAAAGGCAGGATCCTGGGTGGTGGCCCTGAA
TCCTGATTTGTCTGCCCTGCCAGCGAGACACATGTGGTCAAAGATGAATTTGAGAAAAGT
AGCTGCTGGCTACTTGAACAATGGAGGAACACGGCCATCATGAGATGGAAGGCACCCCAT
TGGGTGTCACTCCCACATTAACTGCTGAAGATCAACAGGGAACATCTGGTCACCAACA
TTCGGAACACTCAGTGTCTGGTGGACAACTTGCTGGAGAATGGCTACTTCTCAGCCGAAG
ATGCAGAGATTGTGTGTGCCTGTCCCACCAAGCCTGACAAGGTCCGAAAGATCCTTGACC
TGGTGCAGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCTCTACGTGCTGCAGCAGCTGG
AGGATGCTTACGTGGACCTCAGGCTGTGGCTCTCAGAAATTGGCTTCTCCCCTTCCCAGC
TCATTTCGGACCAAACACTATCGTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGC
GACACCAACTGGGCCGCGACTCCAAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTGC
TGCTGGAGGAGACCTATATGGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAAACC
TGGGCAGCCTAGGAGGCCTGGATTGCCTGCTGGACCACAGTACGGGCGTCCTCAACGAGC
ATGGCGAGACTGTCTTCGTGTTTCGGGGACGCGGGAGTGGGCAAGTCCATGCTGCTGCAGA
GGTTGCAGAGCCTCTGGGCGTCAGGCAGGTTGACCTCCACAGCCAAATTCTTCTTCCACT
TCCGCTGCCGCATGTTTCAAGTCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTGC
TCTTCAAGCATTTCTGCTACCCGGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGCTGC
GCTTTCCCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTCG
ACCTGAGCCGCGTGCCGGATAGCTGCTGCCCCTGGGAGCCGGCTCACCTCTGGTCCTGC
TGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGCCGGCAAATTGCTCACTGCTCGCA
CAGGCGTGGAGGTCCCCCGCCAGCTCCTGCGCAAAAAGGTGCTGCTCCGGGGCTTCTCCC
CAAGTCACCTGCGCGCCTATGCCCCGCGGATGTTCCCCGAGCGCACAGCGCAGGAGCATC
TGCTGCAGCAGCTGGATGCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCT
GTTGGATCATCTTCCGTTGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCAC
AGTTGCCGACTGTGCTGTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATC
TGAACAGGCCGCGAGCCAGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGGCGGAAACCC
TACGTGCAGGCTGGCGCACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCGACA
AGAGCCTCTTTGTGTTTGGCCAGGAGGAGGTGCAGGCGTCGAAGCTGCAGGAAGGAGATC
TGCAGCTGGGCTTCTGCGGGCTTTGCCCGATGTGGGCCCTGAGCAGGGCCAGTCTTACG
AATTTTCCACCTTACGCTCCAGGCCTTCTTACCGCCTTCTTCTTGGTAGCAGATGACA
AAGTGAGCACCCGGGAGTTGCTGAGGTTCTTTCGAGAATGGACGTCTCCTGGAGAGGCAA

FIG. 15A

CAAGCTCGTCCTGCCATTCTTCCTTCTTCTCCTTCCAGTGCCTGGGCGGCAGAAGCCGGT
TGGGCCCTGATCCTTTTCAGGAACAAAGATCACTTCCAGTTCACCAACCTCTTCGTGTGCG
GGCTACTGGCCAAAGCCCGACAGAACTCCTTCGGCAGCTGGTGCCCAAGGCTATCCTGA
GGAGGAAGCGCAAGGCCCTGTGGGCTCACCTGTTTGCTAGCCTGCGCTCCTACTTGAAGA
GCCTACCTCGGGTCCAGTCTGGAGGCTTTAACCAGGTGCATGCCATGCCACATTCTGT
GGATGCTGCGCTGCATCTATGAGACGCAGAGCCAGAAGGTGGGGCGCCTCGCCGCCAGGG
GCATCAGTGCGGACTACCTCAAGCTGGCCTTTTGCAACGCTTGCTCTGCGGACTGCAGCG
CCCTGTCCTTCGTCTCCTGCATCACTTCCACAGGCAGCTGGCCCTAGACCTGGACAACAACA
ACCTCAATGACTATGGCGTGCAGGAGCTGCAGCCTTGCTTTAGCCGTCTCACGGTTATCA
GACTCAGCGTCAACCAGATCACCGACACGGGGGTGAAGGTGCTATGTGAGGAACTGACCA
AGTATAAGATCGTGACGTTCTTGGGTTTATACAACAACCAGATAACTGATATCGGAGCCA
GGTATGTGGCCCAAATCCTGGATGAATGCAGAGGCCTCAAGCACCTTAAACTAGGGAAAA
ACAGAATAACAAGTGAGGGCGGGAAGTGTGTGGCTTTGGCTGTGAAGAACAGCACCTCCA
TCGTTGATGTTGGGATGTGGGGTAATCAGATTGGAGACGAAGGGGCAAAGGCCTTCGCAG
AGGCATTGAAGGACCACCCAGCCTGACCACTCTCAGTCTTGCAATTCATGGCATCTCTC
CGGAGGGAGGGAAGAGCCTTGCGCAGGCCCTGAAGCAGAACACCACACTGACAGTAATCT
GGCTGACCAAAAATGAACTTAATGATGAGTCTGCAGAGTGCTTCGCTGAGATGCTGAGAG
TGAACCAGACGCTACGGCATTATGGCTGATCCAGAATCGCATCACAGCCAAGGGGACAG
CGCAGCTGGCGAGGGCACTGCAGAAGAACACAGCCATAACAGAGATTTGTCTCAATGGAA
ACTTGATTAAGCCCGAGGAGGCCAAAGTCTTCGAGAATGAGAAGAGAATCATCTGCTTCT
GACGGACGCTCCTGGGCAGGATCTTTGTCCTAGGTTGCTCCTCAGTCACAGACAGCACTG
TGCAGTCAGCAGGGTAGCAGGATGCTGTGCAGCGCCTGCAGCAAGGTGCCTGTCAGGAGC
CCACACCTCCACAGTGCACACCGATGTCCCCTGCTCATGCTTGGACTGGTAGCACCCGCG
CCGCGGCTGAGACCCTGCAGACGCAGGGAGTCTTAGGAACCATCGTCACCACTCAAAGCC
AGCAGGGCATCTTCTGTACAAAGATCTCCCTGCATATCCACTAGACGGAAGCTGAAGGAA
CGCAACAGCAGAGGAGGCCAACAGACGCCTGGCTGAAGGCTCCGTGGGACCAACGGTGTG
ACCTTCAGAAAAGAGCTGGGAACTTGAGCAGAGCCGATGGTAACTTCTTGGGGAAAGAAG
GCACCCAGTGACTGCATGGTTATTCTGAGTCTCCTTCTCTGCTTAGTCCCTCTCACTG
TACAGGTCTGTTTCTTCTCGCAGCTGTGGCTGCTGAAGTAGGTCCACTGTGGGGAGAGC
TCATCACAGACTTTGGTTTCGGTTCTGGATTCTCAGTGGTGGCAACCGAGAGTCAGACGAT
ACCCTCTAGGTCAGTCTCAGAGGATCTCTATGCTGTGAGAGGGTTGAGGGCCACCCAGA
ATTTTTTTTTTTTACCAGTTTTTACTGTGCCTGCCCCAGGAGGGAGAATTACTTCCCAGC

FIG. 15B

CTCCACAGCAGCAGGCATGGCTTGCCTCAATGGTCCTGAGATCCCAACAAAACCTCTCTCC
CTTGCCTGTGAGCAGAAAGTATCTTCATGTCCTCAGAAGTTGGAGGGTGACTGGACACAG
TTAAGACTCAGAGAGCCAGCTGATAGCTCAAAGCAAAGCATGGCACATACCCACCACCAT
ACCATGGTGCGCATGGGATGGGACAGTTGGAATGTTGCAGATAACGTGTTCTTTTGCCAG
TTCATTTGTTAATAAAAATATTTAAACGTTAAAAAAGGGCG
G (SEQ ID NO:43)

FIG. 15C

MEEHGHHEMEGTPLGCHSHIKLLKINREHLVTNIRNTQCLVDNLLENGYFSAEDAEIVCA
CPTKPKDKVRKILDLVQSKGEEVSEFFLYVLQQLDAYVDLRLWLSEIGFSPSQLIRTKTI
VNTDPVSRYTQQLRHQLGRDSKFMLCYAQKEDLLEETYMDTLMGLVGFNENLGS LGGL
DCLLDHSTGVLNEHGETVVFVG DAGVGKSM LLQRLQSLWASGRLTSTAKFFFHFRCRMFS
CFKESDMLS LQDLLFKHFCYPEQDPEEVFSFLLRFPHTALFTFDGLDELHSDFDLSRVPD
SCCPWEP AHP LVLLANLLSGRLLKGAGKLLTARTGVEVPRQLLRKKVLLRGFS PSHLRAY
ARRMFPERTAQEHL LQQLDANPNLCSLCGVPLFCWII FRCFQHFQTVFEGSSS QLPDCAV
TLTDVFL LVTEVHLNRPQPSSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLFVFG
QEEVQASKLQEGDLQLGFLRALPDVGPEQGQSYEFFH LTLQAFFTAFFLVADDKVSTREL
LRFFREWTSPGEATSSSCHSSFFSFQCLGGRSRLGPD PFRNKDHFQFTNLFVCGLLAKAR
QKLLRQLVPKAILRRKRKALWAHLFASLSYLKSLPRVQSGGFNQVHAMPTFLWMLRCIY
ETQSQKVGR LAARGISADYLKLAFCNACSA DCSALS FVLHHFHRQLALDLDNNNLNDYGV
QELQPCFSRLTVIRLSVNQITDTGVKVLCEELTKYKIVTFLGLYNNQITDIGARYVAQIL
DECRGLKHLKLGNRITSEGGKCV ALAVKNSTSIVDVGMWGNQIGDEGAKAF AEALKDHP
SLTTL SLAFNGISPEGGKSLAQALKQNTTTLTVIWLTKNELNDESAECFAEMLRVNQTLRH
LWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRIICF
(SEQ ID NO:44)

FIG. 16

mCARD4Lpep . PRO	10	20	30	40	50	60	70	80	90
hCARD4Lpep . PRO	10	20	30	40	50	60	70	80	90
mCARD4Lpep . PRO	100	110	120	130	140	150	160	170	180
hCARD4Lpep . PRO	100	110	120	130	140	150	160	170	180
mCARD4Lpep . PRO	190	200	210	220	230	240	250	260	270
hCARD4Lpep . PRO	190	200	210	220	230	240	250	260	270
mCARD4Lpep . PRO	280	290	300	310	320	330	340	350	360
hCARD4Lpep . PRO	280	290	300	310	320	330	340	350	360
mCARD4Lpep . PRO	370	380	390	400	410	420	430	440	450
hCARD4Lpep . PRO	370	380	390	400	410	420	430	440	450
mCARD4Lpep . PRO	460	470	480	490	500	510	520	530	540
hCARD4Lpep . PRO	460	470	480	490	500	510	520	530	540

FIG. 17A

mCARD4L pep . PRO	LLRFFQEWTPGGAASSCHSSFLSFQCLGGSGRAGEDLFKNKDHQFTNLFVCGLLAKAKQKLLRQLVPAAALRRKRKALWAHLFASLR	550	560	570	580	590	600	610	620	630
hCARD4L pep . PRO	LLRFFREWTPGEATSSSCHSSFFSFQCLGGRSRLGPDPRNKDHQFTNLFVCGLLAKARQKLLRQLVPKAILRRKRKALWAHLFASLR	629								
	LLRFFQEWMPAGAAATTCYPPFLPFQCLQSGSPAREDLFKNKDHQFTNLFVCGLLSKAKQKLLRHLVPAAALRRKRKALWAHLFSSLR	629								
mCARD4L pep . PRO	GYLKS LPRVQVGGFNQVQAMP TFLWMLRCIYETQSQKVGQLAARGISADY LKLAFCNACSADCSALSFVLHFFHKQLALDLNNNLNDYG	640	650	660	670	680	690	700	710	720
hCARD4L pep . PRO	SYLKS LPRVQSGGFNQVHAMP TFLWMLRCIYETQSQKVGRLAARGISADY LKLAFCNACSADCSALSFVLHFFHRQLALDLNNNLNDYG	719								
	GYLKS LPRVQVESFNQVQAMP TFLWMLRCIYETQSQKVGQLAARGICANY LKLTTCNACSADCSALSFVLHFFPKRLALDLNNNLNDYG	719								
mCARD4L pep . PRO	VQELQPCFSRLTVLRLSVNQITDGGVKV LSEELTKYKIVTFLGLYNNQITDVGARYVAQILDECKGLTHLSL YNNQITDVGAKLGKKNKIT	730	740	750	760	770	780	790	800	810
hCARD4L pep . PRO	VQELQPCFSRLTVIRLSVNQITDTGVKVLCEELTKYKIVTFLGLYNNQITDIGARYVAQILDECRGLKHL-----KLGNKIT	797								
	VRELQPCFSRLTVLRLSVNQITDGGVKV LSEELTKYKIVTYLGLYNNQITDVGARYVTKILDECKGLTHLSL YNNQITDVGARLGKKNKIT	809								
mCARD4L pep . PRO	SEGGKYVALAVKNSTSIVDVGMGNQVDEGAKAF AEALKDHPSLTTL SLASNGISTEGGKSLAQALQQNTSLTVLWLTQNELNDEVAES	820	830	840	850	860	870	880	890	900
hCARD4L pep . PRO	SEGGKCV ALAVKNSTSIVDVGMGNQIGDEGAKAF AEALKDHPSLTTL SLAFNGISPEGKSLAQALQNTTTLTVIWLTKNELNDESAEC	887								
	SEGGKYLA LAVKNSKSISEVGMGNQVDEGAKAF AEALRNHPSLTTL SLASNGISTEGGKSLARALQQNTSLEILWLTQNELNDEVAES	899								
mCARD4L pep . PRO	LAEMLKVNQTLKHLWL IQNQITAKGTAQ LADALQSNITGITEICLNGNL IKPEEAKVFEDEKRIICE	910	920	930	940	950	960			
hCARD4L pep . PRO	FAEMLRVNQTLRHLWL IQNRITAKGTAQ LARALQKNATITEICLNGNL IKPEEAKVFENEKRIICE	953								
	LAEMLKVNQTLKHLWL IQNQITAKGTAQ LADALQSNITGITEICLNGNL IKPEEAKVFEDEKRIICE	965								

FIG. 17B

gatcatcggtcactgcagccttgaactcttgtgctcatgtgatcctcctgccttagcctcccca
tagctgggactacaggtgcgccaccatgcctggctaattttttttatttttgttagagatgggtgt
ctcactatgttgacaggttggtctcaaactactggccttacttcaagctatctacccatctcag
cctcccaaagcgctgggattacagtcagagccaacttgccctggccagataaaaggtcttaagcat
ggttccttctgctctaggttagagaaaccccaaccagtgagggtggggtgagctcttctgt
agcttttgctttgctgatgatgtcattgatctcttcaggggctgcgcagagtagcaggggcccctg
gagggcgccgctgaatcctgattgcccttctgctgagaggacacacgcagctgaagatgaattt
gggaaaagtagccgcttgctactttaactatggaagagcagggccacagtgagatggaaataatc
ccatcagagctctacccccacattcaattactgaaaagcaatcgggaaacttctggctactcacat
ccgcaatactcagtgcttggtggacaacttgctgaagaatgactacttctcgccgaagatgcgg
agattgtgtgtgcctgccccaccagcctgacaaggtgccccggggacagggacgggcatggcat
tgtgtggaccccgaggagctagaagaggcctctccctgctgatctgagtgaagagcgtgggagttt
agtccagcgggacgggctgcattttggggtactaatagcacacaaatgcctgggttagcaggttg
cacagtcaggtattttacttctgtgtttgtgtctggagcaaaccctgacatctcagttctcattg
ctgtgtgtattgggtcccagacacttcatttttagatcccctttaaattaggagggaagaaagaac
ataagcataagagcatccccagcagcagtggtcattcagtgccctctgaaggctggagggctgctt
gttgcctgggtgagactcggaggggaaccgactcaggggtcaggaatgatgacatcccacgggtgggt
ccacagtgagaatcttccccgctccactgtgggacgccttaacagcccttacttccacttacgc
tttgcggtatctcctgaaaaataaaaatggagaccacaaattccttcttggttagaggaatgacac
aactcatttatgacatgaccccgctgggactcagaagagaccaggacgggttctgggggaagcag
tagcacactcgtgtgctttgttctcttctcttgatttgtttccacatttttaacaagaaaaaa
agccgtttttaatatatggcctatcgccctcctactgtgtggcccaggtgcctacctcattatgc
ccaaggggtggttctcacctctccactctcattcctgcacagcagttgtgtcaggttaagaggga
caaggagaaggctgggcaccgtggctcacgcctgtaatcccagcactttgggagggccgaggcagg
cagatcacctaagggtcaggagtttgagaccagcctggccaacatggggaaaaccgctctctaata
aaaacacaaaaaattagtcgggcatggtgggtgggtgcctgtaatcccagccacttgggagggctgag
gaaagagaattccttgaacctgggaggtggaggttgagtgagccaagattgtgccattgcactc
cagccctccagcctgggtgacagagcaagactctgtctcaaaaaagaaaaaaaaaaaaaagaggt
agagaagtcacatgggtatttctgtctccttttatttttaggctcatggaagcctcctgggttct
tagagctgagtggttttatttctgtcaggaggtcatttcacagatttccgggctccaatatgt
tgactgtcacagcagctgggggggatggcatagctaccggctgtactaagaactcagagccctgcc
ctgagcctgcctgaggggtccttatggtaggagatgcccctcatgccagccgctgcctcatgct
tgtgtcacctccaggtccgcaaaattctggacctggtacagagcaaggcgaggaggtgtccgag
ttcttctctacttgctccagcaactcgcagatgcctacgtggacctcaggccttggctgctgga
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FIG. 18A

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FIG. 18B

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FIG. 18C

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FIG. 18D

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FIG. 18E

agggacacttaagtctgcagaggttactgctgtctttttgtttgtctgtgcccctgccccagagg
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FIG. 18F

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FIG. 18G

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FIG. 18H

caccaccactgactgtgcaaggcacaacgcaggggtggtttctgtttattcctccagcaaccctgc
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FIG. 18I

tattgtgtgatacacgagtgtgtgctatgaacacaccttgggaaggagtgtgagaggatccttaa
cattttacctgtgtacttttgtcttcctccttttcaacagcctaaatggaaacctgataaaacca
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FIG. 18J

1 GTCGACCCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAAGG
CAGCTGGGTGCGCAGGCCGTCGTCCGTCCGACGTCGTCCGCTCGTTCGTTCTCATTTTCC

63 TGACCGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCACGAGATGCCATCCTGGACGCTCTT
ACTGGCGCCGACGGGTGGGGTCTCGGTACCCCGCCCGTGCTCTACGGTAGGACCTGCGAGAA

1 M G R A R D A I L D A L

125 GAAAACTTGTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
CTTTTGAACAGTCCCTACTTGAGTTTTTCAAGTTCTACTTCGACGACTGTCACGTTGACGC

13 E N L S G D E L K K F K M K L L T V Q L R

187 AGAAGGCTATGGGCGCATCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCACTG
TCTTCCGATACCCGCGTAGGGTGCGCCCCGGGACGACGCTCTACCTGCGGTATCTAGAGTGAC

33 E G Y G R I P R G A L L Q M D A I D L T

249 ACAAACTTGTGTCAGTACTATCTGGAGTCGTATGGCTTGGAGCTCACAATGACTGTGCTTAGA
TGTTTGAACAGTCGATGATAGACCTCAGCATACCGAACCTCGAGTGTTACTGACACGAATCT

54 D K L V S Y Y L E S Y G L E L T M T V L R

311 GACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGAAGAGTCTGGAGCTGT
CTGTACCCGAATGTCTCGACCGACTCGTCGACGTTTGCTGATTTCTTCTCAGACCTCGACA

75 D M G L Q E L A E Q L Q T T K E E S G A V

373 GGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGGACACTTTGTGGACCAGC
CCGTCGACGTCGGTCACAGGGACGAGTCTCATGTCCGTCTTGTCTGTGAAACACCTGGTCG

95 A A A A S V P A Q S T A R T G H F V D Q

435 ACAGGCAAGCACTCATTGCCAGGGTCACAGAAGTGGACGGAGTGCTGGATGCTTTGCATGGC
TGTCGGTTCGTGAGTAACGGTCCCAGTGTCTTACCTGCCTCACGACCTACGAAACGTACCG

116 H R Q A L I A R V T E V D G V L D A L H G

497 AGTGTGCTGACTGAAGGACAGTACCAGGCAGTTTCGTGCAGAGACCACGCAAGACAAGAT
TCACACGACTGACTTCCTGTCATGGTCCGTCAAGCACGTCTCTGGTGGTGGTTCTGTTCTA

137 S V L T E G Q Y Q A V R A E T T S Q D K M

559 GAGGAAGCTCTTCAGCTTTGTTCCATCCTGGAACCTGACCTGCAAGGACTCCCTCCTCCAGG
CTCCTTCGAGAAGTCGAAACAAGGTAGGACCTTGGACTGGACGTTCTGAGGGAGGAGGTCC

157 R K L F S F V P S W N L T C K D S L L Q

621 CCTTGAAGGAAATACATCCCTACTTGGTGATGGACCTGGAGCAGAGCTGAGGTATCTTTTCC
GGAACCTCCTTTATGTAGGGATGAACCACTACCTGGACCTCGTCTCGACTCCATAGAAAAGG

178 A L K E I H P Y L V M D L E Q S

683 AGCTACATTATCTAGCTCCTGACTTTGTATACACAATTTTGAACCAATTTGTATTTGT
TCGATGTAATAGATCGAGGACTGAAACATATGTGTTTAAACCTTTTGTGTTAAACATAAACA

745 GTTTAAAAAAAAAAAAAAAAAGGGCGGCGCGC
CAAATTTTTTTTTTTTTTTTTTCCCGCGGCGC

FIG. 19

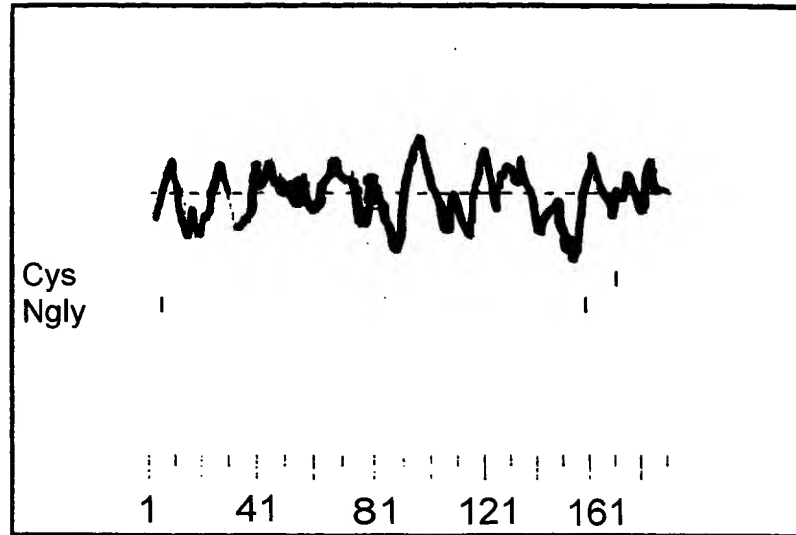


FIG. 20

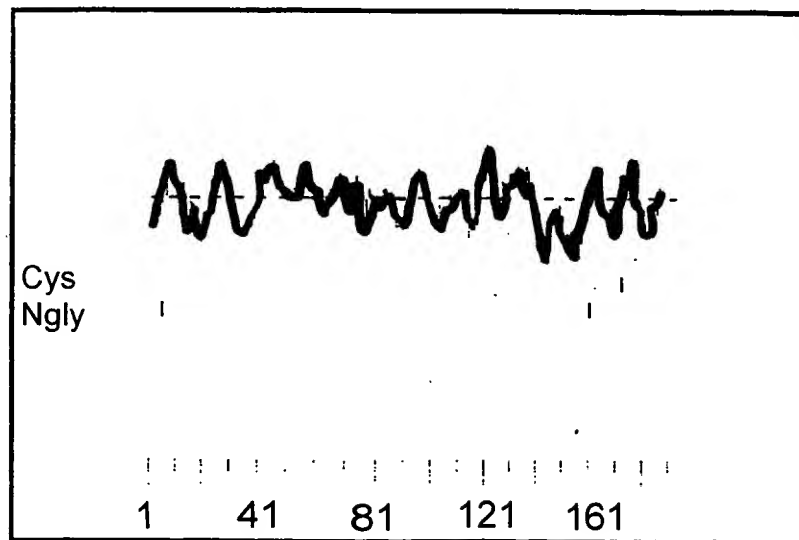


FIG. 22

1 CGCGTCCGGCTGCAGCGGGGTGAGCGGGCGCAGCGGCCGGGGATCCTGGAGCCATGGGGC
CGCGAGGCCGACGTCGCCCCACTCGCCGCCGTCGCCGGCCCCCTAGGACCTCGGTACCCCG
1► M G

61 GCGCGCGCGACGCCATCCTGGATGCGCTGGAGAACCTGACCGCCGAGGAGCTCAAGAAGT
CGCGCGCGCTGCGGTAGGACCTACGCGACCTCTTGGAAGTGGCGGCTCCTCGAGTTCTTCA
3► R A R D A I L D A L E N L T A E E L K K

121 TCAAGCTGAAGCTGCTGTGCGGTGCCGCTGCCGAGGGCTACGGGCGCATCCCGCGGGGCG
AGTTGACTTCGACGACAGCCACGGCGACGCGCTCCCGATGCCCGCGTAGGGCGCCCCCG
23► F K L K L L S V P L R E G Y G R I P R G

181 CGCTGCTGTCCATGGACGCCTTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGA
GCGACGACAGGTACCTGCGGAACCTGGAGTGGCTGTTGACACAGTCGAAGATGGACCTCT
43► A L L S M D A L D L T D K L V S F Y L E

241 CCTACGGCGCCGAGCTCACCGCTAACGTGCTGCCGACATGGGCCTGCAGGAGATGGCCG
GGATGCCCGCGGCTCGAGTGGCGATTGCACGACGCGCTGTACCCGGACGTCCTCTACCGGC
63► T Y G A E L T A N V L R D M G L Q E M A

301 GGCAGCTGCAGGCGGCCACGCACCAGGGCTCTGGAGCCGCGCCAGCTGGGATCCAGGCCC
CCGTCGACGTCCGCGCGGTGCGTGGTCCCGAGACCTCGGCGCGGTGACCCCTAGGTCCGGG
83► G Q L Q A A T H Q G S G A - A P A G I Q A

361 CTCCTCAGTCGGCAGCCAAGCCAGGCCTGCACTTTATAGACCAGCACCGGGCTGCGCTTA
GAGGAGTCAGCCGTCGGTTCGGTCCGGACGTGAAATATCTGGTTCGTGGCCCCGACGCGAAT
103► P P Q S A A K P G L H F I D Q H R A A L

421 TCGCGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTACGGGAAGGTCCTGACGG
AGCGCTCCCAAGTGTGTTGCAACTCACCGACGACCTACGAGACATGCCCTTCAGGACTGCC
123► I A R V T N V E W L L D A L Y G K V L T

481 ATGAGCAGTACCAGGCAGTGCGGGCGGAGCCACCAACCCAAGCAAGATGCGGAAGCTCT
TACTCGTCATGGTCCGTCACGCCCCGGCTCGGGTGGTTGGTTCTACGCCTTCGAGA
143► D E Q Y Q A V R A E P T N P S K M R K L

541 TCAGTTTCACACCAGCCTGGAAGTGGACCTGCAAGGACTTGCTCCTCCAGGCCCTAAGGG
AGTCAAAGTGTGGTCCGACCTTGACCTGGACGTTCTGAAACGAGGAGGTCCGGGATTCCC
163► F S F T P A W N W T C K D L L L Q A L R

601 AGTCCCAGTCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTTCCCAGCAACAC
TCAGGTCAGGATGGACCACCTCCTGGACCTCGCCTCGACTCCGAGGAAGGGTCGTTGTG
183► E S Q S Y L V E D L E R S

661 TCCGGTCAGCCCCCTGGCAATCCACCAAATCATCCTGAATCTGATCTTTTTATACACAAAT
AGGCCAGTCGGGGACCGTTAGGGTGGTTTAGTAGGACTTAGACTAGAAAAATATGTGTGTA

721 ATACGAAAAGCCAGCTTGAA
TATGCTTTTCGGTCGAACTT

FIG. 21

ALIGN calculates a global alignment of two sequences

version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

> hCARD5-DNA 740 aa vs.

> mCARD5-DNA 763 aa

scoring matrix: paml20.mat, gap penalties: -12/-4

68.2% identity; Global alignment score: 2377

```

              10      20      30
inputs C---GCGTCCGGCTGCAG-CGGGGTG-----AGCG-GCGGCAGC-----GGC
      :  ::::::::::: :::: :  .::: ::::::::::: :::
      CCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAGGTGAC
              10      20      30      40      50      60

              40      50      60      70      80      90
inputs CGGGGAT-----CCTGGAGCCATGGGGCGCGCGCGCAGCCATCCTGGATGCGCTGGA
      :: :: :  :: ::::::::::::::: ::::: :: ::::::::::: :: :: ::
      CGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCACGAGATGCCATCCTGGACGCTCTTGA
              70      80      90      100     110     120

              100     110     120     130     140     150
inputs GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGTCGGTGCCGCTGCG
      .::: .::: :  :: ::::::::::::::: ::::::::::: ::::::::::: :::::::::::
      AAACCTTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
              130     140     150     160     170     180

              160     170     180     190     200     210
inputs CGAGGGCTACGGGCGCATCCCCGCGGGGCGCGCTGCTGTCCATGGACGCCTTGGACCTCAC
      ::::::::::: ::::::::::: :::: :::: :::: :::: :::: :::: :::: ::::
      AGAAGGCTATGGGCGCATCCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCAC
              190     200     210     220     230     240

              220     230     240     250     260     270
inputs CGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTACCGCTAAC-GTGC
      ::::::::::: ::::::::::: ::::::::::: ::: :::: :::: :::: :::: ::::
      TGACAAACTTGTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCAC-AATGACTGTGC
              250     260     270     280     290

              280     290     300     310     320     330
inputs TGC GCGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCCACGCACCAGGGCT
      :  : ::::::::::: ::::::::::: ::::: ::::::::::: : : : :::: :
      TTAGAGACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGA--AGAG-T
      300     310     320     330     340     350

              340     350     360     370     380     390
inputs CTGGAGCCGCGCCAGCTGGGATCCAGGCCCTCCTCAGTCGGCAGCCAAGCCAGGCCTGC
      ::::::::::: : : ::::::::::: .. : . : ::::: ::::::::::: ::::::::::: ::::: :
      CTGGAGCTGTGGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGG---AC
              360     370     380     390     400     410

              400     410     420     430     440     450

```

FIG. 23A


```

      690      700      710      720      730      740
inputs AAATCATCCTGAATCTGATCTTTTTATACACAATATACGAAAAGCCAGCTTGAA
      :::  :  :::::::::::  : :::::  .  :::::  :  :::::
      AATTTTGA AAAACAATT-TGTATTGTGTTTAAAAAAAAAAAAAAAAAAGG
              720      730      740      750      760

```

FIG. 23B

FIG. 24

1 CCCGCGTCCGGA CTTCCTTCCAGTGT TTTGTTCTCTCTGCTCTCTCCAACAGAAGGTATTTTGG
GGGCGCAGGCCTGAAGGGAAGGTCACAAACAAGGAGAGACGAGAGAGGTTGTCTTCCATAAAAAAC

66 GCATGTTTTATCTTTTGCTAAGTAGGATTTCTGTCTTTCTTTGTTAACACAGATTTCTTTCTGTGC
CGTACAAAATAGAAACGATTTCCTTAAAGACAGAAAGAAACAATTGTGTCTAAAGAAAGACAGC

131 CAGAATGACCTGATCCATTTCTGTTTGTAGAAAGCCATGGCTTCAGAGGGTGTCTTCTCAGAA
GTCTTACTGGACTAGGTAAAGGACCAAAACATCTTTCCGTACCGAAGTCTCCACGAAGGAGTCTT
----- 1 M A S E G A S S E -----

196 ATCATAGAAAAACAGCGAACAAAGTTGCTCAGTGTCTTCCAACAAGATCCCGACTCTATCTTGA
TAGTATCTTTTTGTGCTTGTTCACAGAGTCACAGGAGGTTGTCTAGGGCTGAGATAGAACCT
----- 10 I I E K Q R T K L L S V L Q Q D P D S I L D -----

261 CACGTTAACCTCTCGGAGACTGATTTCTGAGGAGGAGTATGAGACTCTAGAGGCAATTACAGATC
GTGCAATTGGAGAGCCTCTGACTAAAGACTCTCTCTCATACTCTGAGATCTCCGTTAATGTCTAG
----- 31 T L T S R R L I S E E E Y E T L E A I T D -----

326 CTCTGAAGAAAAGCCGGAAGCTGTTAATTTTGATCCAGAAGAAGGGAGAGGACAGCTGTTGTGTG
GAGACTTCTTTTCGGCCTTCGACAATTAAACTAGGTCTTCTTCCCTCTCTGTGCGACAACAACA
----- 53 P L K K S R K L L I L I Q K K G E D S C C C -----

391 TTCCTCAAGTGTCTGTCTAATGCCTTTCCACAGTCAGCTTCCACCTTGGGTTTAAAGCAGGAAGT
AAGGAGTTACAGACAGATTACGGAAGGTGTGAGTCAAGGTGGAACCCAAATTTCTGCTCTCA
----- 75 F L K C L S N A F P Q S A S T L G L K Q E V -----

456 TCCACGGCAGGGGACTGGAGAGGTTGTGAGGTGAGCAGGGGTTTGGAAGATCCCTTTTCTCTTG
AGGTGCGCTCCCTGACCTCTCCAACAGCTCCACTCGTCCCCAAACCTTCTAGGGAAAAGAGAAC
----- 96 P R Q G T G E V V E V S R G L E D P F S L -----

521 GGACCATAACCCAGAAATAGCAGAGCTCTCAGAAGAGAAAGAATGCCCGGTCTGGGAGCTCCG
CCTGGTATTGGGGTCTTTATCGTCTCGAGAGTCTTCTCTTTCTTACGGGCCAGACCCTCGAGGC
----- 118 G T I T P E I A E L S E E K E C P G L G A P -----

586 GAGTTCTTACCTGCAAGGAAAGCAGCCACAGGGAACCGGAAGTACCTTCTTGGGAGAATCAGGA
CTCAAGAAGTGGACGTTCTTTCTGTCGGTGTCCCTTGGCCTTCATGGAAGAACCCTCTTAGTCCT
----- 140 E F F T C K E S S H R E P E V P S W E N Q E -----

651 AGGGCGTGGTGCACAGCAAGTCACCGCTCCGCGTTCAGTCAAAGGAGTTGAGTATGAAGTTCCAG
TCCCGCACCAAGTGTGCTTCAAGTGGCGAGGCGCAAGTCAAGTTTCTCAACTCATACTTCAAGGTC
----- 161 G R G A Q Q V T A P R S V K G V E Y E V P -----

FIG. 25A

716 CAAGTATCTCCCTCTTAAGCGACGGGCAGAGATACGAGGAGCCAGATGATTGCTGTACTTAGAA
GTTTCATAGAGGGAGAATTTCGCTGCCCGTCTCTATGCTCCTCGGTCTACTAAGCGACATGAATCTT
183▶ A S I S L L S D G Q R Y E E P D D S L Y L E

781 GAAGGGGAAGGTGAAGAGTCTCTTGGGTACCCTGAAGATGTTTTGGAGGAAGGGGCCGGCGATGA
CTTCCCCCTTCCACTTCTCAGAGAACCCATGGGACTTCTACAAAACCTCCTTCCCCGGCCGCTACT
205▶ E G E G E S L G Y P E D V L E E G A G D D

846 CCCACAGTGCTTTGTATATGATAGTGAGGAGGAATGCGAGTATGAGGAAAACATGGGCTCCTCCG
GGGTGTCACGAAACATATACTATCACTCCTCCTTACGCTCATACTCCTTTTGTACCCGAGGAGGC
226▶ P Q C F V Y D S E E E C E Y E E N M G S S

911 GTGAAGACAGTAGCTGCGACGACACTTCAGAGACCTGCGTTCCATTGGAAGGGGAGAAAAGCGCT
CACTTCTGTGTCATCGACGCTGCTGTGAAGTCTCTGGACGCAAGGTAACCTTCCCCCTCTTTTCGCGA
248▶ G E D S S C D D T S E T C V P L E G E K S A

976 GAAGAAAGAAAAAGAGTGTTC AACACGTCCTGTCTGTTCGAACATGGATAGAAACAGAAAGCT
CTTCTTTCTTTTCTCACAAGTTGTGACGAGCAGGACAAACTTGTACCTATCTTTGTCTTTTCGA
270▶ E E R K R V F Q H V L S C L N M D R N R K L

1041 TCTCCCAGAGTTTCGTGAGGCAGTTTTCATAGACCGAGGATGTGAGTGGACACCCAAGACCCAG
AGAGGGTCTCAAGCACTCCGTCAAAAGGTATCTGGCTCCTACACTCACCTGTGGGTTCTGGGGTC
291▶ L P E F V R Q F S I D R G C E W T P K T P

1106 GAGACTTAGCTTGGAATTTCTTGATGAAAGTTCAGGCTTTAGACTCGACAGCCAGAGATTCTATC
CTCTGAATCGAACCTTAAAGAACTACTTTCAAGTCCGAAATCTGAGCTGTGGTCTCTAAGATAG
313▶ G D L A W N F L M K V Q A L D S T A R D S I

1171 CTGAGGCCCGAGGTGGCGGGTGAAGAGAATGAAGAATTGCCGGCTGGAATAGAGAAGTTAGGCAT
GACTCCGGGCTCCACCGCCCACTTCTCTTACTTCTTAACGCGCGACCTTATCTCTTCAATCCGTA
335▶ L R P E V A G E E N E E L P A G I E K L G I

1236 TGGAGACCCCCAAACCATCCATCCCCTGGATGTCCTCTGCGCCTGCATGCTTTGTGCAGACAGCT
ACCTCTGGGGGTTTGGTAGGTAGGGGACCTACAGGAGACGCGGACGTACGAAACACGTCTGTCTGA
356▶ G D P Q T I H P L D V L C A C M L C A D S

1301 CCTTGACGCGTGAAGTCATGTCAAACATGTACCAATGCCAGTTTGCTCTTCCCCTGCTACTGCCA
GGAACGTCGCACTTCACTACAGTTTGTACATGGTTACGGTCAAACGAGAAGGGGACGATGACGGT
378▶ S L Q R E V M S N M Y Q C Q F A L P L L L P

1366 GATGCTGAGAACAAACAAAACCTCTTAATGGTAGGGGCCATGAAGGACTTAAAGCAGCCCTCAGC
CTACGACTCTTGTTGTTTGGAGAATTACCATCCCCGGTACTTCTGAATTTGTCGGGAGTCG
400▶ D A E N N K N L L M V G A M K D L K Q P S A

FIG. 25B

1431 ACAGTCCTCAGGAGGGCCCTCAGGGAAACAGACACATTTCTGGGTCTCACAAAGATGCCTGTCA
TGTCAGGAGTCTCCCGGGGAGTCCCTTTGTCTGTGTAAAGACCCAGAGTGTTCCTACGGACAGT
... 421▶ Q S S G G P L R E T D T F L G L T K M P V ...

1496 TCTCTTTTGTGCGACTAGGACGCTGCAGCTTCTCCAAGTCCAGAATTGTTAACACACTGCTCAGC
AGAGAAAACACGCTGATCCTGCGACGTCGAAGAGGTTTCAGGTCTTAACAATTGTGTGACGAGTCG
... 443▶ I S F V R L G R C S F S K S R I V N T L L S ...

1561 TCCTCCCAGCAGAAACCATACCCGATTTTCCTCCATCAGGATCTGTCTGTCCCTGTGCTTCCTCG
AGGAGGGTCTGCTTTTGGTATGGGCTAAAAGGAGGTAGTCTTAGACAGACAGGGACACGAAGGAGC
... 465▶ S S Q Q K P Y P I F L H Q D L S V P V L P R ...

1626 GCAAATTTCTGACGGCCTGGTGGAAGTGACATGGTGCTTTCTGACAAGTTGCTGAAGGAAAGCC
CGTTTAAAGACTGCCGGACCACCTTCACTGTACCACGAAAGGACTGTTCAACGACTTCCTTTTCGG
... 486▶ Q I S D G L V E V T W C F P D K L L K E S ...

1691 CGCATGCTTTCCAGAAACCTGTTGCTGTGGCCAACCTTCGTGGAGATTTAGAAAGCTTTTGGATA
GCGTACGAAAGGTCCTTTGGACAACGACACCGGTTGGAAGCACCTCTAAATCTTTTCGAAAACCTAT
... 508▶ P H A F Q K P V A V A N L R G D L E S F W I ...

1756 CAATTTGGTTTCTCGGTAGAAGTTTCTCCGGTCTTTTCTTTTTCACAGACTGCCTTGGTGAGAA
GTTAAACCAAAGGACCATCTTCAAAGGAGGCCAGAAAAGAAAAGTGTCTGACGGAACCACTCTT
... 530▶ Q F G F L V E V S S G L F F F T D C L G E K ...

1821 GGAATGGGACTTGCTAATGTTTTTAGGAGAGGACACCATTGAACGGTGCTACTTTATCCTCAGTC
CCTTACCCTGAACGATTACAAAAATCCTCTCCTGTGGTAACTTGCCACGATGAAATAGGAGTCAG
... 551▶ E W D L L M F L G E D T I E R C Y F I L S ...

1886 CCCAGGCTAAGGAGAGTGAAGAAGCCCAGATTTTCCAAGGATCCTAAAACCTGAAGCEATCTCAG
GGGTCCGATTCTCTCACTTCTTCGGGTCTAAAAGGTTTCCTAGGATTTTGACTTCGGTAGAGTC
... 573▶ P Q A K E S E E A Q I F Q R I L K L K P S Q ...

1951 CTACTGTTTTGGGAAGCTGAGGAAGCTGGGGATAGAAGGAAGACTATGGAGGCCCTTCAAGCTGC
GATGACAAAACCTTCGACTCCTTCGACCCCTATCTTCCTTCTGATACCTCCGGGAAGTTCGACG
... 595▶ L L F W E A E E A G D R R K T M E A L Q A A ...

2016 CCTCCAGGAAGTAATGTCCTCTCCACTCAGATGTGTGTCCCTTGAAGAGATGGCCTCTCTGGCCA
GGAGGTCTTTCATTACAGGAGAGGTGAGTCTACACACAGGGAACTTCTCTACCGGAGAGACCGGT
... 616▶ L Q E V M S S P L R C V S L E E M A S L A ...

2081 GGGAGCTGGGCATTTCAGGTAGACCAAGACTTTGAAGTTACTCAAGATATTCAAGTTTCCCCACA
CCCTCGACCCGTAAGTCCATCTGGTTCTGAAACTTCAATGAGTTCTATAAGTTCAAAGGGGGTGT
638▶ R E L G I Q V D Q D F E V T Q D I Q V S P T

FIG. 25C

2146 ACAGTTGAAGGTGAAAACCAACAACCATGTAGTCAGACCAAAGCCCGGCTGAAAGCGGAGCTCA
TGTCAACTTCCACTTTTGGTTGTTGGTACATCAGTCTGGTTTTCGGGCCGACTTTCGCCTCGAGT
... 660▶ T V E G E N Q Q P C S Q T K S P A E S G A Q ...

2211 GGAGCCAATCAGAGAGCCAGGGGCTCAATGTGACGACAGTCAGAATGCTCCGGTTTTCATCAGA
CCTCGGTTAGTCTCTCGGTCCCCGAGTTACACTGCTGTGAGTCTTACGAGGCCAAAAGGTAGTCT
... 681▶ E P I R E P G A Q C D D S Q N A P V F H Q ...

2276 CTCCAGTATACATGCCTTATCCAGCACACCCATGGGCTTTGGCCATCAAAGCTGGAGGTAACTTT
GAGGTATATGTACGGAATAGGTCTGTGGGTACCCGAAACCGGTAGTTTCGACCTCCATTGAAA
... 703▶ T P V Y M P Y P A H P W A L A I K A G G N F ...

2341 TACCACGTTCCCTTTGAATGCCCCCTGGTTATGGGCTCCCACTTTGGATCACAGCAGAGGGCTAAG
ATGGTGCAAGGAACTTACGGGGGACCAATACCCGAGGGTGAAACCTAGTGTCTCTCCCGATTCT
... 725▶ Y H V P L N A P W L W A P T L D H S R G L S ...

2406 TGGTTCTTTCCATTCCCATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAACTGCCACCATC
ACCAAGAAAGGTAAAGGTACGATTGGGTGAGTGAGATTCCGGAAGGTTGATTGACGGTGGTAG
... 746▶ G S F H S H A K P T H S K A F Q A N C H H ...

2471 CCCATCCCTCCCATGCTAAACCCACTCATGTGAATCCCTCTCATGCTAAACCCACTCATGTGCAG
GGGTAGGGAGGGTACGATTGGGTGAGTACACTTAGGGAGAGTACGATTGGGGTGAAGTACACGTC
... 768▶ P H P S H A K P T H V N P S H A N P T H V Q ...

2536 CCTTGATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAAACCCACTCCCTCTCAGACCTCT
GGAACGTACGATTGGGTGAGTGAGATTCCGGAAGGTTGATTGGGTGAGGGAGAGTCTGGAGA
... 790▶ P C M L N P L T L R P S K L N P L P L R P L ...

2601 TGGAGCCAAGCTAACTGCAATCATGCCATCCCTCCCTTGCTAAACCCCTCTCATACGAATCCCTC
ACCTCGGTTGATTGACGTTAGTACGGGTAGGGAGGGAACGATTGGGAGAGTATGCTTAGGGAG
... 811▶ G A K L T A I M P I P P L L N P L I R I P ...

2666 TGATGCTAACCCCACTCATGTGCAGCCTTCCCATGCTAAACCCGCTCATCTACAGTCTTCCCAA
ACTACGATTGGGGTGAAGTACACGTCGGAAGGGTACGATTGGGGCAGTAGATGTCAGAAGGGTTT
... 833▶ L M L T P L M C S L P M L N P L I Y S L P K ...

2731 CAAAACCTCCCCATCCCAATCTACTGCAGTTACGGGCACACAAACCTCAGCAGTCCCAGTCTAA
GTTTTGGGAGGGGTAGGGTTAGATGACGTCAAGTGCCGTGTGTTGGAGTCGTGAGGGTCAGATT
... 855▶ Q N P P H P N L L Q F T A H K P Q Q S Q S K ...

2796 GCCTTCTCAGCAGAGACCCAGTCAGCCTAAATCATTCCAGACCAAGCCTTACAGGCCAGGGCCT
CGGAAGAGTCGTCTCTGGGTGAGTCGATTAGTAAGGTCTGGTTCGGAAGTGTCCGGTCCCGGA
876▶ P S Q Q R P S Q P K S F Q T K P S Q A R A

FIG. 25D

2861 GCCACCCAAGAGCAGGGAGACGTTAAAGAACATACTCTGGAGATCTGGGAAATAAAGTATGGGCT
CGGTGGGTTCCTCGTCCCTCTGCAATTTCTTGTATGAGACCTCTAGACCCTTTATTTTCATACCCGA
898▶ C H P R A G R R -----

2926 TTGCTTAAGTATTCTTTTTTCATATAGCAAGCTGAAGAAAAGTTTTAGTGAAAGACTGATAAAAGT
AACGAATTCATAAGAAAAGTATATCGTTCGACTTCTTTTCAAAATCACTTTCTGACTATTTTCA-----

2991 AGCAAAACCCAAAAAGGTATGCAAAGTCTTAAAGTGCATAGCAAAGTATCCAAGTGTGGGAAATA
TCGTTTTGGGTTTTTTCCATACGTTTCAGAATTCACGTATCGTTTCATAGGTTACACCCCTTTAT-----

3056 TGGAAGCAGTTAAAAGTAGAATCTGGCTGGGCATGGTGGCACACATCTACAGGGTTTTAGCATGGG
ACCTTCGTC AATTTTCATCTTAGACCGACCCGTACCACCGTGTGTAGATGTCCCAAATCGTACCC-----

3121 AGGGCTCTGTCTATCCCAACTCAGAGAAGCAGGCAGATCTCTGTGTGTTTGAGGCCAGTCTGGTCT
TCCCGAGACAGTAGGGTTGAGTCTCTTCGTCCGTCTAGAGACACACAACTCCGGTCAGACCAGA-----

3186 ACATAACAACGACACAAGCAAGTCCTACATCAGCCATACTACAAAATGAGACCCCATCTGGGGAC
TGTATTGTGTGCTGTGTTTCGTTTCAGGATGTAGTCGGTATGATGTTTTACTCTGGGGTAGACCCCTG-----

3251 AAAAGGGTTGGATCTAACATCAAACCAAGAAATCAGTCAAGTATTCCAGAAGGCATCATTAAAT
TTTTCCCAACCTAGATTGTAGTTGGTTTCTTTAGTCAGTTCATAAGGTCTTCCGTAGTAATTAA-----

3316 ACACTCAGTGGGTTACCACAACCAACCATACTCGACAACCTAACCCCTAAAGGAGCAAGAAGGA
TGTGAGTCACCCAATGGTGTGGTTTGGTATGACCTGTTGATTGGGGGATTTCTCTGTTCTTCCT-----

3381 GTTGGGTGGGTGTTAGGCTGAACATGATTGGGGAAGAACTGAAGATAGATAAGGTCAATTCGTAAT
CAACCCACCCACAATCCGACTTGTACTAACCCCTTCTTGACTTCTATCTATTCCAGTAAGCATTA-----

3446 ACAGGTTATGGGACTTGTCAAATCCATTAAATGCAATATTAAGAAGCAGTGGGAATCTTAAGGCT
TGTCCAATACCCCTGAACAGTTTAGGTAATTTACGTTATAATTCCTTCGTCACCCTTAGAATTCGGA-----

3511 ACATTAAGCTCCAGTGAGTCGCAACCCCTCCCCTATTAGATGATGTGAGATTTGAACCCCACTGAA
TGTAATTCGAGGTCACCTCAGCGTTGGGAGGGGATAATCTACTACACTCTAAACTTGGGGTCACCT-----

3576 TGGGGTGTGTCTGATAGCCCGTGTGTGTGACAACTGTGTAATTATAAAGTGATGAAAACGTGGG
ACCCACACAGACTATCGGGCACACACTGTTTGACACATTAATATTTCACTACTTTTGCACCC-----

3641 AGTTCAGCTTATCTGTGTTGAAGAAAGGCTGCTTCAGAGGTGCCTTGGTTTTGGGTTTATGATCA
TCAAGTCAATAGACACAACCTTCTTTCCGACGAAGTCTCCACGGAACCAAAACCAATACTAGT-----

FIG. 25E

3706 GCCACTGAGCAGATACTCTGCACCATTGGTACAGTTAAATCAGCTTGCTTCTGGTAATAGCCCCA
CGGTGACTCGTCTATGAGACGTGGTAACCATGTCAATTTAGTCGAACGAAGACCATTATCGGGGT

3771 ATCTACCACATTTATCCCTTACAGGCGGAAATAATGAATGATCAGCAAAACATCCAATTTTACCT
TAGATGGTGTAAATAGGGAATGTCCGCCTTTATTACTTACTAGTCGTTTTGTAGGTTAAATGGA

3836 TAACCTTGGTACTGATTTGTATATGTATCATTCTTTATATAATAGCTAAGAAAAATTTAGCTCATT
ATTGGAACCATGACTAAACATATACATAGTAAGAAATATATTATCGATTCTTTTAAATCGAGTAA

3901 AGGGGTCTGATATATTAGTTTAAATGGTTTGAAGTCAGAAATGTGTTAGTTTAAATTTTAGAGT
TCCCAAGACTATATAATCAAATTACCAAACTTCAGTCTTTACACAATCAAAAATTTAAATCTCA

3966 TAATTGAAAAATATTGAGATGAATTTACAAAGGCTATAAGTAATGTTTGAGAGGGTTATAATTTTT
ATTAACTTTTATAACTCTACTTAAATGTTTCCGATATTCAATTACAACTCTCCCAATATTAAAAA

4031 GTAGACTCATACTGTTCTGAACATTTGGATAGCTTCTCGTAGTTAGCAGTGTATAGAAGAATAT
CATCTGAGTATGACAAGACTTGTAAACCTATCGAAGAGCATCAATCGTCACAAATCTTCTTATA

4096 ATTTGATTTCAGGTATTTAACCAGAGCTGCTCTTAGTTTTTAAGTGTACCAAGAGTCAATAAAAG
TAAACTAAGTCCATAAATTGGTCTCGACGAGAATCAAAAATTCACAGTGGTTCTCAGTTATTTTC

4161 GCTACATTATCTGAACATGTGGGAACACAACCTGTGACCTTACACTTAAGAGACTGAGGAAGGGAA
CGATGTAATAGACTTGTACACCCTTGTGTTGACACTGGAATGTGAATTCTCTGACTCCTTCCCTT

4226 ATCAAGGTTCAAGCCAGCAGCACATAGTGAGACCAGGTCTCAAGACACAAAACTATCCACCTTA
TAGTTCCAAGTTCGGTCGTCGTGTATCACTCTGGTCCAGAGTTCGTGTTTTTGTAGGTGGAAT

4291 AGGAAGATTTTAAAAATTTGCCTCATTAAGAAATAAAGTAAGATTTATAAATTGGACTAAAATGTCA
TCCTTCTAAAAATTTAAACGGAGTAATCTTTATTTTCAATTCATAATTTTAACTGATTTACAGT

4356 CATCTTTGAACTTATGACTGTTTAAATTTTTTGAAGTTTAAATTTTATTATTGTATGCGTGT
GTAGAACTTGAATACTGACAAATTAaaaaaactGAATTTCAAATTTAAATAAATACATACGCACA

4421 GTTGTATGTGTGTGCACATGTGTGCCACTGCATGTATGTGGAGGCCATCAGACAATGTTGTAGAG
CAACATACACACACGTGTACACACGGTGACGTACATACACCTCCGGTAGTCTGTTACAACATCTC

4486 TCTGTTCTTTCTCTTAGCCCTATGTGTTTTACCCACTGAGCTAGGCCACCTACTCCTATAAGTC
AGACAAGAAAGGAGAATCGGGATACACAAAATGGGTGACTCGATCCGGTGGATGAGGATATTTCAG

FIG. 25F

4551 TAATTTTAAATAGTAAATAGTTCTAAGAAGTCAATCAGGGAAAAAATGGCTGTCAAAGTCTCA
ATTAAATTTATCATTTTATCAAGATTCTTCAGTTAGTCCCTTTTTTTACCGACAGTTTCAGAGT

4616 AAGAAAAATCGTATTAGCCATGGATAGAGACTCACCTCTTGAATCATTGTGTCTGAGAATAGCC
TTCTTTTATAGCATAATCGGTACCTATCTCTGAGTGGAGAACTTAGTAAACACAGACTCTTATCGG

4681 TAATATCACAATAATGTGTTTGTACATGTGTTAGTTAATATTGTTTTTCAGAGTATTTAATCTCTC
ATTATAGTGTATTATACACAAACATGTACACAATCAATTATAACAAAAGTCTCATAAATTAGAGAG

4746 ATGATTATTGTAAAGATGAAAAAGAAATAGTGGGCAATGTATGTGAGTATTTAATTTTGCCTGA
TACTAATAACATTTCTACTTTTTTCTTTATCACCCGTTACATACACTCATAAATTAAACGGACT

4811 CAATTCGTCTTTTAGAATGATAAATGTAAGAAGTAAAAATAAACGGTTTCATTCTCAGAACAACT
GTTAAGACAGAAAATCTTACTATTTACATTCTTCATTTTATTTTGCCAAGTAAGAGTCTTGTGTA

4876 AAGCCAGCTCACTTAAGTCTGGGCCCTGCTGGCATTGGCTAGTCTAGCTACCCCCACCCAAACAC
TTCGGTCGAGTGAATTCAGACCCGGGACGACCGTAACCGATCAGATCGATGGGGGTGGGTTTGTG

4941 AAAAGTTTAGAGAAGAAAATGACTGAGTCAAGCTTGCCTAATGACTTTTGGACATAAAGTTTATG
TTTTCAAATCTCTTCTTTTACTGACTCAGTTTCGAACGGATTACTGAAAACCTGTATTTCAAATAC

5006 GTCCTAGAAAGCCTTAAAATAAGTAGGATATAAAACATGTAAATTAACCCACACATTATGTGGGT
CAGGATCTTTTCGGAATTTTATTCATCCTATATTTTGTACATTTAATTGGGTGTGTAATACACCCA

5071 TGAGAAGCAGAAAAATGTCAGTAGAACACTCGGCCAGTGCATAAAGAAGGAAGAGACCTCTGTTT
ACTCTTCGTCTTTTACAGTCATCTTGTGAGCCGGTCACGTATTTCTTCTTCTCTGGAGACAAG

5136 TGGGTTATAAAACTGCTCTTTGTGCTCAATTTGTCCCCTGCTTTTGTGTTGCCAGAATGTACAAGA
ACCCAATATTTTGACGAGAAACACGAGTTAAACAGGGGACGAAAACAAACGGTCTTACATGTTCT

5201 TTATAAAATAAACTCACTTTTACTTTTAAAAAATAAAAAAAAAAAGGGCGG
AATATTTTATTTGAGTGAAAATGAAAATTTTTTTTTTTTTTTTTTTTTCCTCCGCC

FIG. 25G

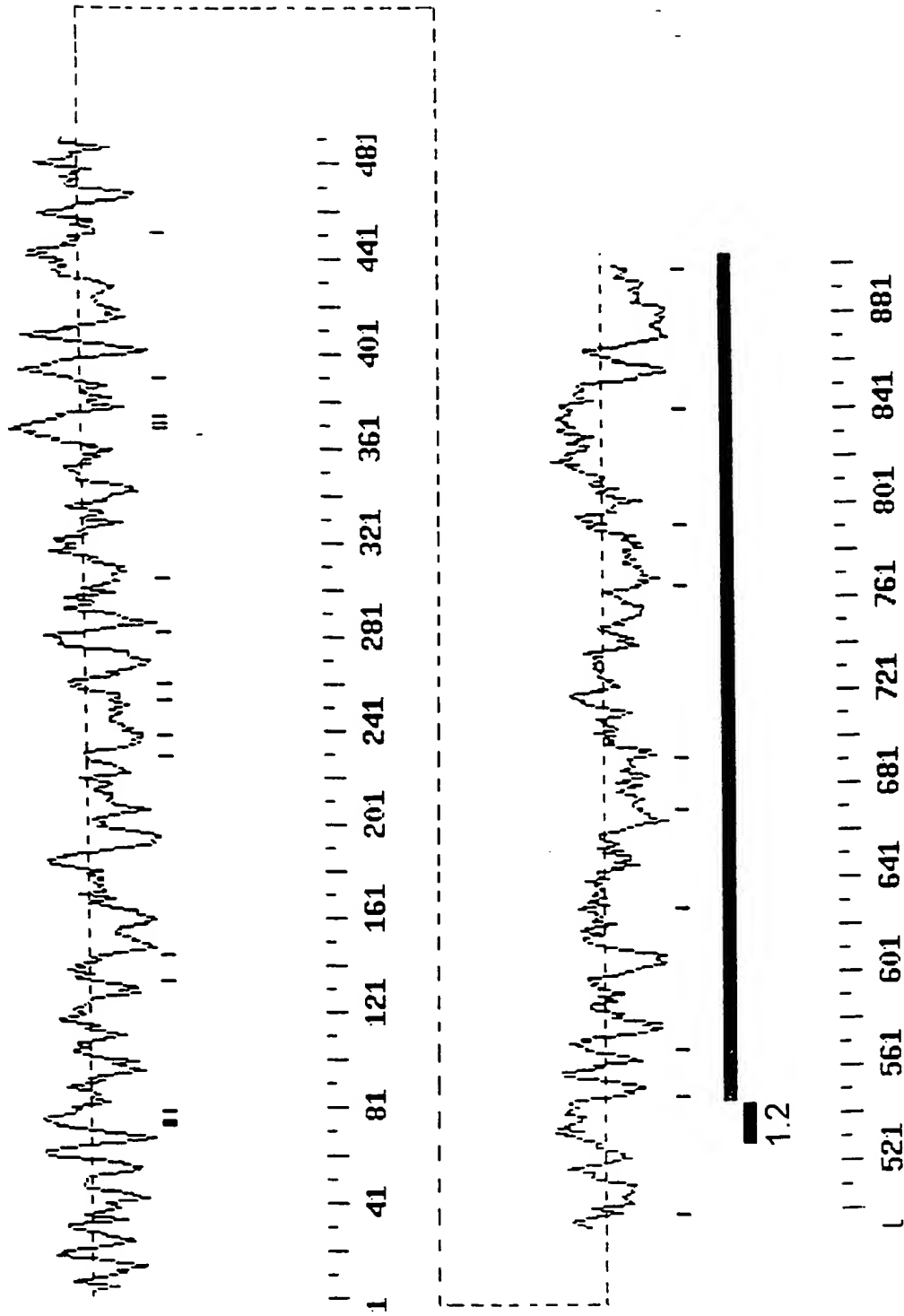
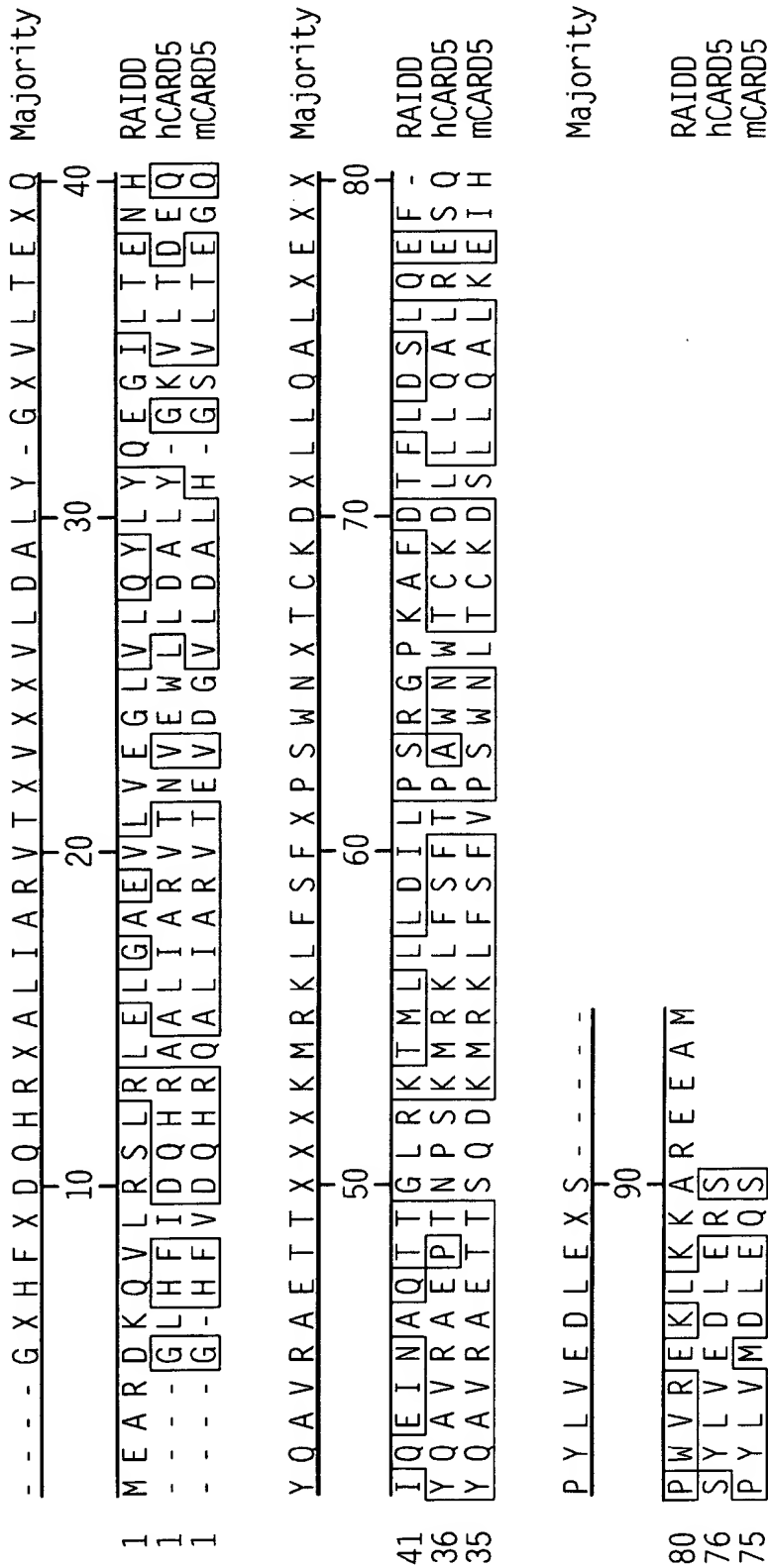


FIG. 26



CACGCGTCCGCCGGATCAGAGAGTGCTCCGAGCTGGGTTGCCCCACTGTGCTTGATCTGCACTCTCCAACACTAGGC 79

ATCATTGACATGTTAAAGCTTAGCCAAATAGAATTGTTCTTTGTGCTTCTTTTTTAACTTTTACTTATTCATTAGGAT 158

M A T E S T P S E 9
GATTTTCATAATATATTTCTCGGTTTAGAGGAAACAGGAACA ATG GCT ACC GAG AGT ACT CCC TCA GAG 226

I I E R E R K K L L E I L Q H D P D S I 29
ATC ATA GAA AGA GAA AGA AAA AAG TTG CTT GAA ATC CTT CAA CAT GAT CCT GAT TCT ATC 286

L D T L T S R R L I S E E E Y E T L E N 49
TTA GAC ACG TTA ACT TCT CGG AGG CTG ATT TCT GAG GAA GAG TAT GAG ACT CTG GAG AAT 346

V T D L L K K S R K L L I L V Q K K G E 69
GTT ACA GAT CTC CTG AAG AAA AGT CGG AAG CTG TTA ATT TTG GTA CAG AAA AAG GGA GAG 406

A T C Q H F L K C L F S T F P Q L A A I 89
GCG ACC TGT CAG CAT TTT CTC AAG TGT TTA TTT AGT ACT TTT CCA CAG TTA GCT GCC ATT 466

C G L R H E V L K H E N T V P P Q S M G 109
TGC GGC TTA AGG CAT GAA GTT TTA AAA CAT GAG AAT ACA GTA CCT CCT CAA TCT ATG GGG 526

A S S N S E D A F S P G I K Q P E A P E 129
GCA AGC AGT AAT TCA GAA GAT GCT TTT TCT CCT GGA ATA AAA CAG CCT GAA GCC CCT GAG 586

I T V F F S E K E H L D L E T S E F F R 149
ATC ACA GTG TTC TTC AGT GAG AAG GAA CAC TTG GAT TTG GAA ACC TCT GAG TTT TTC AGG 646

D K K T S Y R E T A L S A R K N E K E Y 169
GAC AAG AAA ACT AGT TAT AGG GAA ACA GCT TTG TCT GCC AGG AAG AAT GAG AAG GAA TAT 706

D T P E V T L S Y S V E K V G C E V P A 189
GAC ACA CCA GAA GTC ACA TTA TCA TAT TCA GTT GAG AAA GTT GGA TGT GAA GTT CCA GCA 766

T I T Y I K D G Q R Y E E L D D S L Y L 209
ACT ATT ACA TAT ATA AAA GAT GGA CAG AGA TAT GAG GAG CTA GAT GAT TCT TTA TAC TTA 826

G K E E Y L G S V D T P E D A E A T V E 229
GGA AAA GAG GAA TAT CTA GGA TCT GTT GAC ACC CCT GAA GAT GCA GAA GCC ACT GTG GAA 886

E E V Y D D P E H V G Y D G E E D F E N 249
GAG GAG GTT TAT GAT GAC CCA GAG CAC GTT GGA TAT GAT GGT GAA GAG GAC TTC GAG AAT 946

S E T T E F S G E E P S Y E G S E T S L 269
TCA GAA ACC ACA GAG TTC TCT GGT GAA GAA CCA AGT TAT GAG GGA TCA GAA ACC AGC CTT 1006

S L E E E Q E K S I E E R K K V F K D V 289
TCA TTG GAG GAG GAA CAG GAG AAA AGT ATA GAA GAA AGA AAA AAG GTG TTT AAA GAT GTC 1066

L L C L N M D R S R K V L P D F V K Q F 309
CTG TTA TGT TTG AAC ATG GAT AGA AGC AGA AAG GTT CTG CCA GAT TTT GTT AAA CAA TTC 1126

S L D R G C K W T P E S P G D L A W N F 329
TCC TTA GAT CGA GGA TGT AAG TGG ACC CCT GAG AGT CCA GGA GAC TTA GCC TGG AAT TTC 1186

L M K V Q A R D V T A R D S I L S H K V 349
CTG ATG AAA GTT CAA GCA CGA GAT GTG ACG GCT AGG GAT TCA ATC CTC AGT CAC AAG GTT 1246

L D E D S K E D L L A G V E N L E I R D 369
CTG GAT GAA GAT AGC AAG GAG GAT TTG CTG GCT GGA GTG GAG AAT TTG GAA ATT CGA GAC 1306

FIG. 28A

I	Q	T	I	N	P	L	D	V	L	C	A	T	M	L	C	S	D	S	S	389
ATA	CAA	ACC	ATT	AAT	CCC	CTT	GAC	GTG	CTT	TGT	GCC	ACC	ATG	CTG	TGT	TCA	GAT	AGC	TCT	1366
L	Q	R	Q	V	M	S	N	M	Y	Q	C	Q	F	A	L	P	L	L	L	409
TTG	CAA	CGC	CAA	GTC	ATG	TCA	AAC	ATG	TAT	CAG	TGC	CAG	TTT	GCT	CTT	CCC	CTG	CTA	CTG	1426
P	D	A	E	N	N	K	S	I	L	M	L	G	A	M	K	D	I	V	K	429
CCA	GAT	GCA	GAA	AAC	AAC	AAA	AGC	ATC	TTA	ATG	CTG	GGG	GCC	ATG	AAA	GAC	ATT	GTG	AAG	1486
K	Q	S	T	Q	F	S	G	G	P	T	E	D	T	E	K	F	L	T	L	449
AAG	CAG	TCA	ACA	CAG	TTT	TCA	GGG	GGG	CCT	ACA	GAG	GAT	ACA	GAA	AAG	TTT	CTG	ACT	CTC	1546
M	K	M	P	V	I	S	F	V	R	L	G	Y	C	S	F	S	K	S	R	469
ATG	AAG	ATG	CCT	GTC	ATC	TCT	TTT	GTG	CGT	CTA	GGA	TAC	TGT	AGC	TTC	TCT	AAG	TCC	AGA	1606
I	L	N	T	L	L	S	P	A	Q	L	K	L	H	K	I	F	L	H	Q	489
ATC	CTC	AAC	ACA	CTT	CTC	AGC	CCT	GCC	CAG	TTG	AAA	TTA	CAC	AAA	ATC	TTT	CTT	CAT	CAA	1666
D	L	P	L	L	V	L	P	R	Q	I	S	D	G	L	V	E	I	T	W	509
GAT	TTG	CCT	CTT	TTG	GTG	CTT	CCC	CGG	CAA	ATC	TCT	GAT	GGC	CTG	GTT	GAG	ATA	ACA	TGG	1726
C	F	P	D	S	D	D	R	K	E	N	P	F	F	Q	K	P	V	A	L	529
TGT	TTT	CCT	GAT	AGC	GAT	GAT	AGA	AAG	GAA	AAC	CCC	TTT	TTC	CAA	AAG	CCT	GTT	GCT	CTG	1786
A	N	L	R	G	N	L	E	S	F	W	T	Q	F	G	F	L	M	E	V	549
GCT	AAT	CTC	CGT	GGA	AAT	CTA	GAA	AGT	TTT	TGG	ACT	CAG	TTT	GGT	TTT	TTG	ATG	GAA	GTT	1846
S	S	A	V	F	F	F	T	D	C	L	G	E	K	E	W	D	L	L	M	569
TCT	TCA	GCT	GTG	TTT	TTT	TTC	ACT	GAC	TGT	TTA	GGT	GAG	AAG	GAA	TGG	GAC	TTG	CTA	ATG	1906
F	L	G	E	A	A	I	E	R	C	Y	F	V	L	S	S	Q	A	R	E	589
TTT	TTA	GGA	GAG	GCT	GCC	ATT	GAA	AGA	TGC	TAC	TTT	GTT	CTC	AGT	TCC	CAA	GCC	AGG	GAG	1966
S	E	E	A	Q	I	F	Q	R	I	L	N	L	K	P	A	Q	L	L	F	609
AGT	GAA	GAG	GCT	CAA	ATT	TTT	CAG	AGG	ATA	CTG	AAC	TTG	AAG	CCA	GCA	CAG	CTA	CTG	TTT	2026
W	E	R	G	D	A	G	D	R	R	K	N	M	E	G	L	Q	A	A	L	629
TGG	GAG	AGG	GGA	GAT	GCT	GGG	GAT	AGA	AGG	AAG	AAC	ATG	GAG	GGC	CTT	CAA	GCT	GCC	CTC	2086
Q	E	V	M	F	S	S	C	L	R	C	V	S	V	E	D	M	A	A	L	649
CAG	GAA	GTG	ATG	TTC	TCT	TCT	TGC	CTC	AGA	TGT	GTG	TCT	GTG	GAG	GAT	ATG	GCC	GCC	CTG	2146
A	R	E	L	G	I	Q	V	D	E	D	F	E	N	T	Q	R	I	Q	V	669
GCC	AGG	GAG	CTG	GGG	ATT	CAG	GTA	GAT	GAA	GAC	TTT	GAA	AAC	ACT	CAG	AGA	ATT	CAA	GTT	2206
S	S	G	E	N	M	A	G	T	A	E	G	E	G	Q	Q	R	H	S	Q	689
TCC	TCT	GGA	GAA	AAC	ATG	GCT	GGG	ACA	GCT	GAA	GGT	GAG	GGT	CAG	CAA	AGA	CAC	AGT	CAG	2266
L	K	S	S	S	K	S	Q	A	L	M	P	I	Q	E	P	G	T	Q	C	709
CTA	AAA	AGC	TCA	TCT	AAA	AGC	CAG	GCT	CTA	ATG	CCA	ATT	CAA	GAG	CCT	GGG	ACT	CAA	TGT	2326
E	L	S	Q	N	L	Q	N	L	Y	G	T	P	V	F	R	P	V	L	E	729
GAG	CTC	AGC	CAG	AAT	CTT	CAG	AAT	CTC	TAT	GGT	ACC	CCA	GTA	TTC	AGG	CCT	GTT	CTA	GAG	2386
N	S	W	L	F	P	T	R	I	G	G	N	F	N	H	V	S	L	K	A	749
AAC	TCC	TGG	CTC	TTT	CCA	ACC	AGA	ATT	GGA	GGT	AAC	TTT	AAC	CAT	GTT	TCC	TTG	AAA	GCC	2446
S	W	V	M	G	R	P	F	G	S	E	Q	R	P	K	W	F	H	P	L	769
TCC	TGG	GTT	ATG	GGC	CGC	CCC	TTT	GGG	TCA	GAG	CAG	AGG	CCT	AAG	TGG	TTC	CAT	CCT	TTG	2506

FIG. 28B

P F Q N A G A Q G R G K S F G I Q S F H 789
 CCT TTT CAG AAT GCA GGG GCC CAG GGC CGA GGT AAA AGT TTT GGT ATT CAA TCC TTC CAT 2566

P Q I F Y S G E R F M K F S R V A R G C 809
 CCC CAG ATA TTT TAT TCA GGT GAA AGA TTC ATG AAA TTT TCC AGA GTT GCT CGG GGA TGT 2626

H S N G T F G R L P R P I C Q H V Q A C 829
 CAC TCG AAT GGA ACA TTT GGG AGA CTG CCA AGA CCC ATT TGT CAG CAT GTA CAG GCC TGC 2686

P E R P Q M M G T L E R S R A V A S K I 849
 CCT GAG AGA CCA CAA ATG ATG GGA ACT CTT GAA AGG TCT AGG GCA GTA GCC TCC AAG ATA 2746

G H S Y S L D S Q P A R A V G K P W P Q 869
 GGT CAC TCC TAT TCC CTG GAT TCA CAG CCA GCA AGA GCA GTA GGG AAG CCA TGG CCT CAG 2806

Q A C T R V T E L T E A T G K L I R T S 889
 CAA GCT TGC ACC AGG GTA ACA GAG TTA ACT GAA GCA ACT GGA AAA CTG ATA AGA ACA TCC 2866

H I G K P H P Q S F Q P A A A T Q K L R 909
 CAT ATT GGA AAG CCT CAC CCT CAG TCC TTT CAA CCA GCA GCA GCC ACA CAA AAA CTA AGA 2926

P A S Q Q G V Q M K T Q G G A S N P A L 929
 CCT GCT TCT CAG CAA GGA GTC CAG ATG AAG ACA CAA GGT GGG GCT TCA AAT CCA GCT CTC 2986

Q I G S H P M C K S S Q F K S D Q S N P 949
 CAA ATA GGG TCC CAT CCC ATG TGC AAG AGC TCT CAG TTC AAA TCC GAT CAG TCC AAC CCA 3046

S T V K H S Q P K P F H S V P S Q P K S 969
 TCC ACA GTC AAA CAC TCC CAG CCT AAA CCC TTC CAT TCT GTG CCC TCT CAA CCT AAA TCC 3106

S Q T K S C Q S Q P S Q T K P S P C K S 989
 TCT CAG ACA AAA TCC TGT CAG TCC CAG CCC TCC CAA ACT AAA CCT TCT CCA TGC AAA TCT 3166

T Q P K P S Q P W P P Q S K P S Q P R P 1009
 ACT CAG CCT AAG CCA AGC CAG CCC TGG CCT CCC CAG TCT AAG CCT TCT CAG CCC AGA CCC 3226

P Q P K S S S T N P S Q A K A H H S K A 1029
 CCT CAA CCT AAG TCA TCC TCA ACC AAT CCT TCA CAA GCT AAG GCA CAC CAC TCA AAA GCA 3286

G Q K R G G K H * 1038
 GGG CAG AAG AGG GGA GGG AAG CAT TAA 3313

AGAGCTAACTCCAGAGATCTATAAAGCATATCCTTTACCCAGGCCATTCTATCATATAGTAAGCAGAAGAGTTGCCAT 3392

GAAAGTAAAGACTACTGTCTATTAGCATGTAAAACAAAGAAAGATATACATGACCGAATTGGATATCTTTGTTTGTGTTG 3471

TTTGAGACAGAGTTTCACTCTTGTTGCCAGGCTGGAGTGCAATGGCACGATCTCGGCTCACCGCAACCTCTGCTTCCT 3550

GGCTTAAAGTGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCACCACCACACCCAGCTAATTTTG 3629

TATTTTATAGTAGAGGCAGGGTTTCTCCATGTTGGTCAAGCTGGTCTTGAACCTCCCGACCTCAGGTGATCCGCCCACCTA 3708

GGCCTCTCAAAGTGTTGGGATTACGTGTGTAAGCCACAGTGCCCAGCCCGAATTGGATATCTTTAAGATATCTGTAAGT 3787

GTTATATCCCTAACCAAGAAGAAAAATATGAAAATAATTAAGACTAGAATCAAGCAGTAGATAATTGAATCCAATCTTG 3866

GGTATTATTAGATAATGTATAACTTGCACCCAGGGAATGGGGGTCTATGAGACAACCCCACTTGGAGAAGAATGGGGTT 3945

AGGGTCTCTAATTGCAAAGTGACTGTACAATAGGACGAAAGTTGCCTCTGTGTCTGAGAAAGTATCTTAGTTGTTGGCT 4024

FIG. 28C

GCTCCAGAGGTATCTTTGTCAAAAAGCTTCTGTGTTCAATATCAGCCACTGAGCAGATAACCTGCTTATTTGGTGTGGTT 4103
AAATCCAACTAGCTTCTGCTAATAGCCCCCAATTTGCTTGAATGGGAAAACTCTCTCATTGACCCCTTATAGGTAGAAAATA 4182
ATGAATTAA CAACCAATAAAATTATCATTTTGGCATTAAAAAAAATAAAAAAARAAA 4244

FIG. 28D

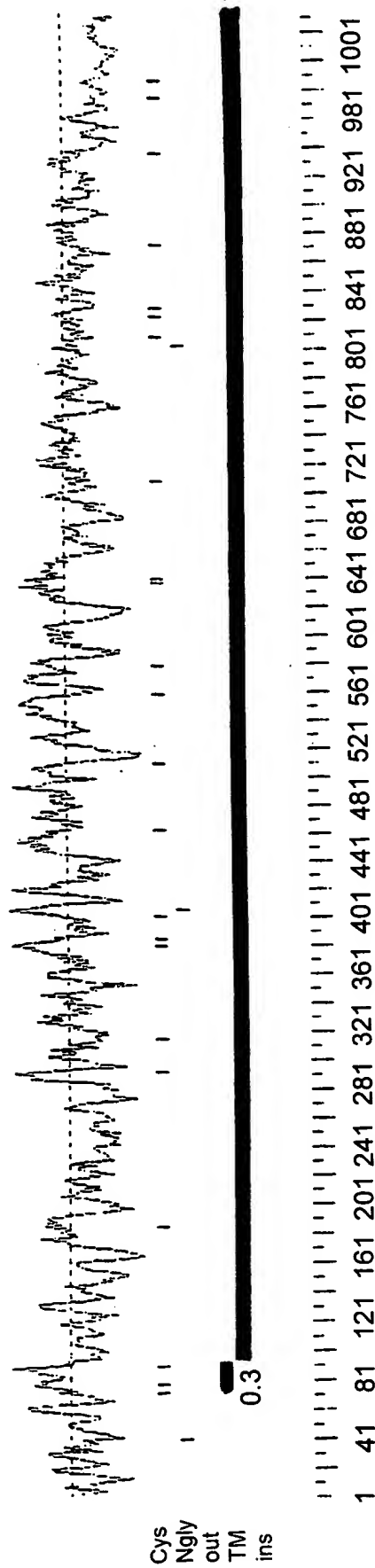


FIG. 29


```
CONSENSUS      *->maederlLkknrvrliesLgldvLdelldvLlekdvlnlkeeEkik  
      +++      +  ++ r++l+e+L+ d +Ld L +++++ ++e E  
CARD6          5      STP--SEIIRERKKLLEILQHD-PDSILDTLTSRRLISEEYETLE 48  
  
CONSENSUS      ragakledDKarelvdsIqrrgsqafdaIdaledTggsyLAdvLel<-*  
      + 1 +      r 1++ +q++g. + ++ f+ +l++      LA++ +l  
CARD6          49 NVTDLLKK--SRKLLILVQKKGEATCQHFLKCLFS-TFPQLAAICGL 92
```

FIG. 30

- A - E S - G S E I I D Q H R X A L L A R V T E D P - D S L L D A L L S R D L I																																								Majority				
10										20										30										40														
1	I	A	Q	Q	W	-	-	-	I	Q	S	K	R	E	D	I	V	N	Q	M	T	E	A	C	L	N	Q	S	L	D	A	L	L	S	R	D	L	I	hCARD3-CARD					
1	-	-	-	-	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	-	Q	C	L	V	D	N	L	L	K	N	D	Y	F	hCARD4-CARD		
1	-	-	-	-	-	-	-	-	G	L	H	F	I	D	Q	H	R	A	L	I	A	R	V	T	N	-	-	V	E	W	L	L	D	A	L	L	Y	G	K	-	V	L	hCARD5-CARD	
1	-	-	-	-	-	-	-	-	G	-	H	F	V	D	Q	H	R	Q	A	L	I	A	R	V	T	E	-	-	V	D	G	V	L	D	A	L	L	H	G	S	-	V	L	mCARD5-CARD
1	M	A	T	E	S	-	T	P	S	E	I	I	E	R	E	R	K	K	L	L	E	I	L	Q	H	D	P	-	D	S	I	L	D	T	L	L	T	S	R	R	L	I	hCARD6-CARD	
1	M	A	S	E	G	A	S	S	E	I	I	E	K	Q	R	T	K	L	L	S	V	L	Q	Q	D	P	-	D	S	I	L	D	T	L	L	T	S	R	R	L	I	rCARD6-CARD		
S E E D Y E A V E A E T T X L L S K V R K L L I L V Q S K G E E T C K - F L K C L																																								Majority				
50										60										70										80														
36	M	K	E	D	Y	E	L	V	S	T	K	P	T	R	T	S	K	V	R	Q	L	L	D	T	T	D	I	Q	G	E	E	-	-	-	-	F	A	F	V	I	hCARD3-CARD			
37	S	A	E	D	A	F	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	E	V	S	E	F	F	L	-	Y	L	hCARD4-CARD			
32	T	D	E	Q	Y	Q	A	V	R	A	E	P	T	N	P	S	K	M	R	K	L	F	S	F	T	P	A	W	-	N	W	T	C	K	-	-	-	D	L	L	hCARD5-CARD			
31	T	E	G	Q	Y	Q	A	V	R	A	E	T	T	S	Q	D	K	M	R	K	L	F	S	F	V	P	S	W	-	N	L	T	C	K	-	-	-	D	S	L	mCARD5-CARD			
40	S	E	E	Y	E	T	L	E	N	V	T	D	L	L	K	K	S	R	K	L	L	I	L	V	Q	K	K	G	E	A	T	C	Q	H	F	L	K	C	L	hCARD6-CARD				
40	S	E	E	Y	E	T	L	E	A	I	T	D	P	L	K	K	S	R	K	L	L	I	L	T	Q	K	K	G	E	D	S	C	C	C	F	L	K	C	L	rCARD6-CARD				
L Q A L K D S A A Y L G L D P E V - - - - - L E - S																																								Majority				
90										100										110										120														
72	V	Q	K	L	K	D	N	K	Q	-	M	G	L	Q	P	Y	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hCARD3-CARD		
76	L	Q	Q	L	A	D	-	-	A	Y	V	D	L	R	P	W	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hCARD4-CARD		
68	L	Q	A	L	R	E	S	Q	S	Y	L	V	E	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hCARD5-CARD			
67	L	Q	A	L	K	E	I	H	P	Y	L	V	M	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	mCARD5-CARD			
80	F	S	T	F	P	Q	L	A	A	I	C	G	L	R	H	E	V	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hCARD6-CARD			
80	S	N	A	F	P	Q	S	A	S	T	L	G	L	K	Q	E	V	P	R	Q	G	T	G	E	V	V	F	V	S	-	-	-	-	-	-	-	-	-	-	-	-	rCARD6-CARD		

FIG. 31